

# 活用 TAIR 於植物研究：阿拉伯芥與作物的實用工具 Using TAIR for Plant Research: Practical Tools for Arabidopsis and Crops



The Arabidopsis Information Resource



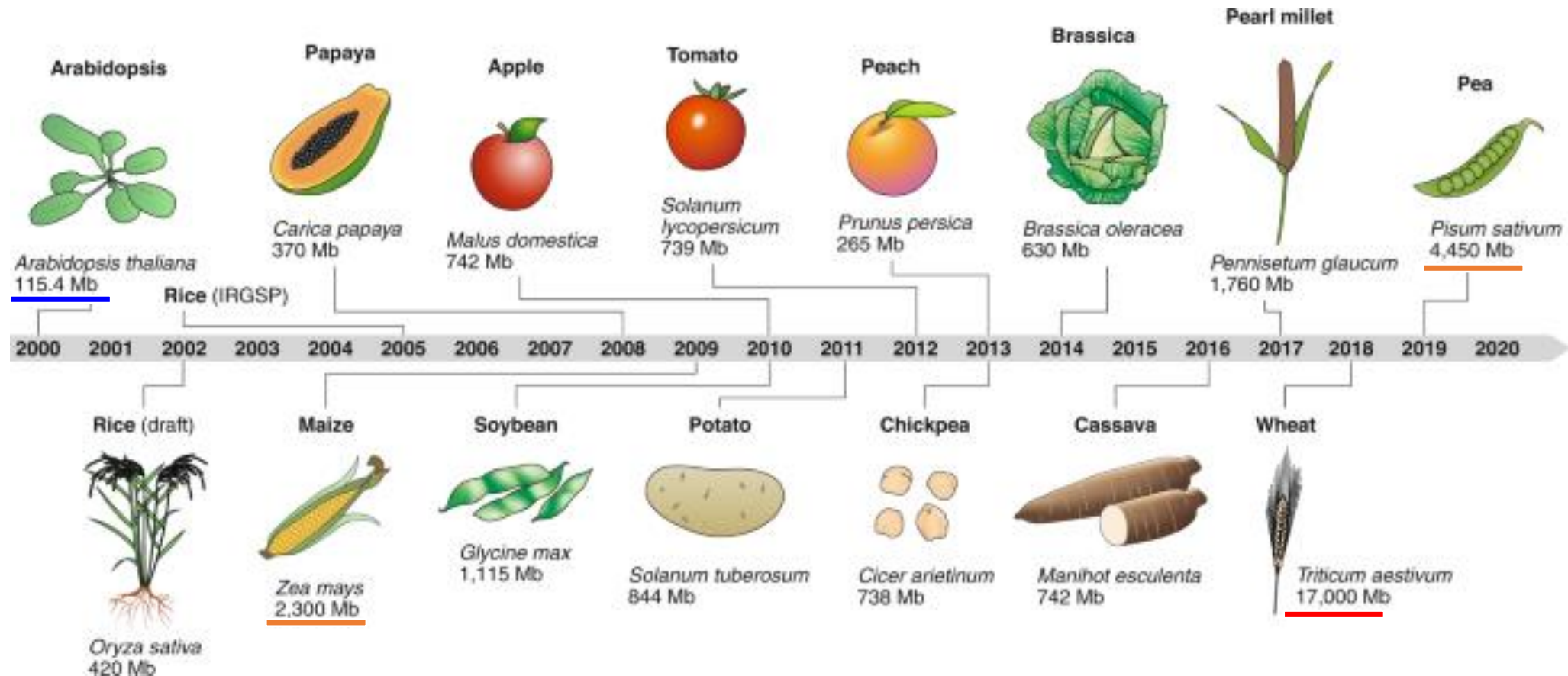
## Ho-Ming Chen (陳荷明)

- Associate fellow, Agricultural Biotechnology Research Center (ABRC), Academia Sinica
- 25 years of experience in bioinformatics
  - Data: Microarray, Small RNA, RNA degradome, RNA-Seq, Ribo-seq
  - Species: **Arabidopsis (model diploid)**, **banana (crop; triploid)**, rice, tomato etc

## Why TAIR database?

- You can do fewer experiments, take fewer wrong turns, and graduate sooner
- You can do biology research from a different perspective, surpass your supervisor, and become a **next-generation** plant researcher.

# Timeline of plant genome release

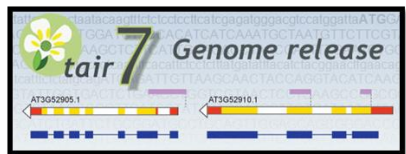
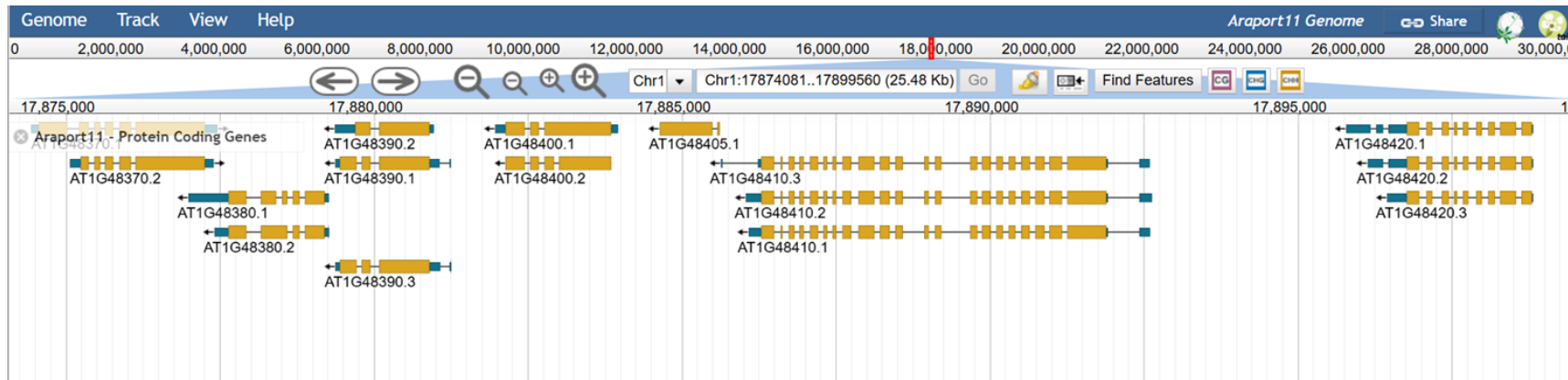


<https://www.nature.com/articles/s41588-021-00866-3>

# Arabidopsis genome annotation

- High quality sequence with few gaps
- High quality of [genome annotation](#) (frequent update)

**Genome annotation:** The process of identifying the locations of genes and all of the coding regions in a genome and determining what those genes do.



# TAIR annotations among versions

All Genome Versions Statistics							
	Protein Coding Genes	Transposons and pseudogenes	Alternatively spliced genes	Gene density (Kb/gene)	Avg. exons per gene	Avg. exon length	Avg. intron length
TAIR10 (11/10)	27,411	4,827	5,885	4.35	5.89	296	165
TAIR9 (6/09)	27,379	4,827	4,626	4.35	5.67	304	165
TAIR8 (4/08)	27,235	4,759	4,330	4.37	5.62	306	165
TAIR7 (4/07)	26,819	3,889	3,866	4.44	5.79	268	165
TAIR6 (11/05)	26,541	3,818	3,159	4.48	5.64	269	164
TIGR5 (1/04)	26,207	3,786	2,330	4.54	5.42	276	164
TIGR4 (4/03)	27,170	2,218	1,267	4.38	5.31	279	166
TIGR3 (8/02)	27,117	1,967	162	4.32	5.24	266	166
TIGR2 (1/02)	26,156	1,305	28	4.48	5.25	265	167
TIGR1 (8/01)	25,554	1,274	0	4.55	5.23	256	168
Nature (12/00)	25,498	NA	NA	4.50	5.20	250	168

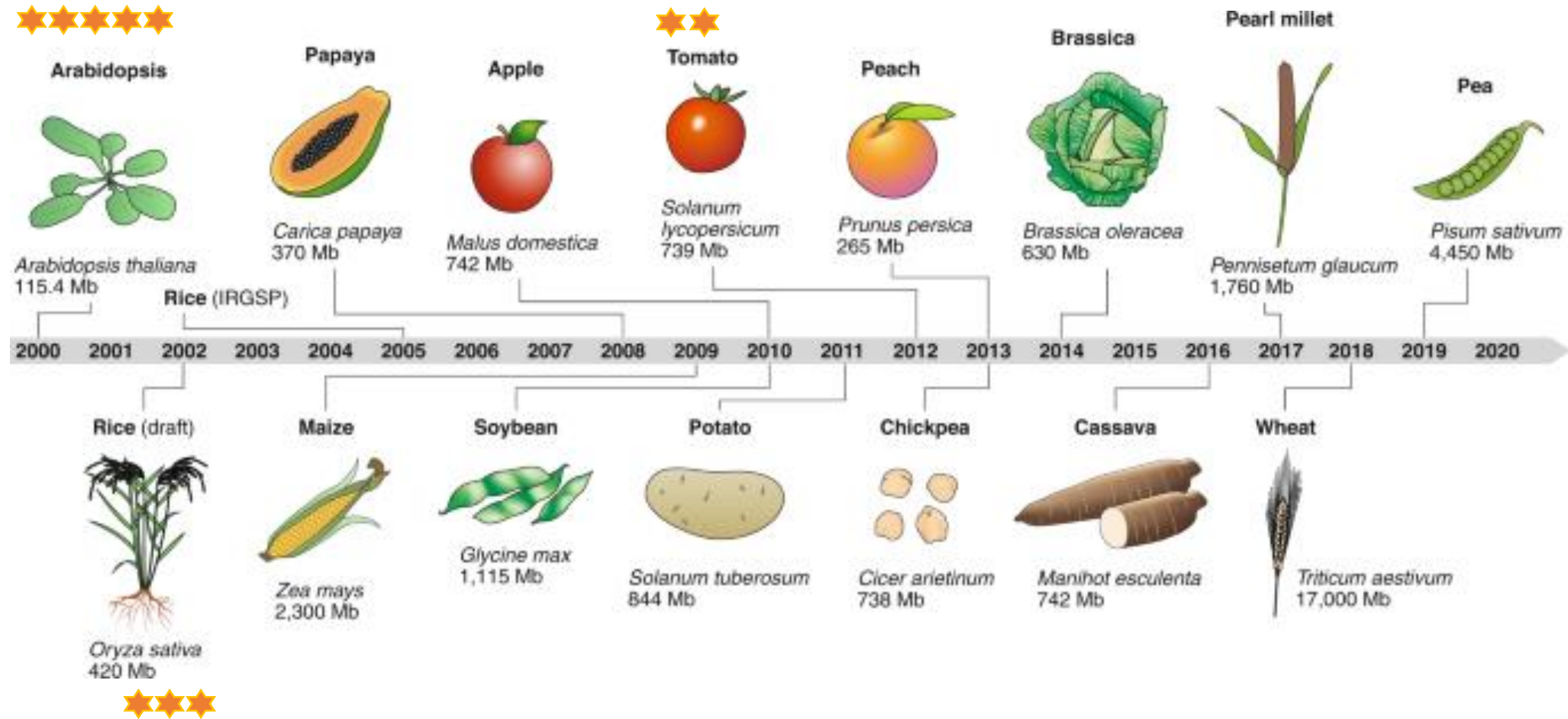
Type	TAIR10	Araport11	Change
(A) Protein-coding genes			
Total number of loci	27 416	27 655 <sup>a</sup>	+239
Number of transcript isoforms	35 386	48 359	+12 973
Number of loci with two or more splice variants	5804	10 696	+4892
Number of loci with changes in CDS	–	–	+1158
Number of loci with changes in UTR(s)	–	–	+21 298
Upstream open reading frame (uORF)	58	84	+26

Cheng et al., (2017) Plant Journal



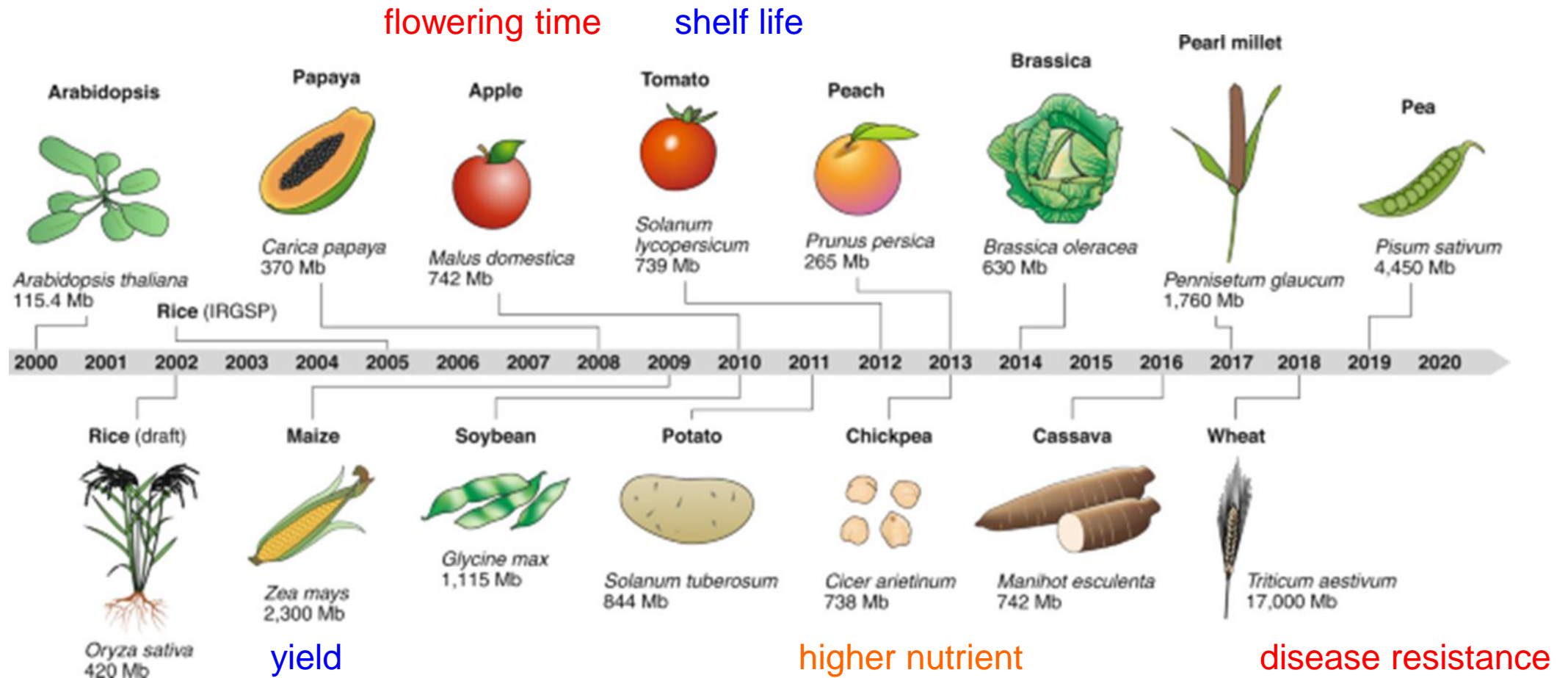
# Quality of plant genomes

## Genome assemblies and annotations



<https://www.nature.com/articles/s41588-021-00866-3>

# Translational agricultural research



# Finding target genes in crops

- Early flowering

ChatGPT ▾

I would like to use genome editing to create an early flowering orange line. Please suggest two targets to edit.

Thought for 12s

Nice — good goal. Below are **two high-confidence gene targets** you can consider editing in orange (Citrus) to promote earlier flowering, with concise rationale, likely phenotypes, and key caveats. I'll keep this at a conceptual, non-actionable level (no editing protocols or sequence/guide design).

## 2) A citrus TFL1 / CEN homolog (e.g., *CsTFL1* / TFL1-like gene) — *loss-of-function / repression*

Why: TFL1 (and CEN/TFL1-like genes) antagonize FT and maintain meristem indeterminacy; loss of TFL1 function typically releases meristems to flower earlier. TFL1 homologs in woody perennials (including citrus) have been identified and linked to flowering control. PMC +1

Expected outcome: earlier and/or more frequent flowering due to reduced repression of floral meristem identity. Combining reduced TFL1 activity with moderate FT activation can be synergistic.

Oxford Academic

Major trade-offs/risks: loss of meristem indeterminacy can change tree form, branching pattern, and possibly long-term productivity. Complete loss-of-function can be more disruptive than controlled down-regulation.

ChatGPT can make mistakes. Check important info.


Read review papers and check TAIR database



# TAIR homepage

subscribed



 **tair**

[Home](#) | [Help](#) | [Contact](#) | [About Us](#) | [Subscribe](#) | [Login](#) | [Register](#) Institution: Academia Sinica (subscribed)

Gene 🔍

[Advanced Search](#) [Browse](#) [Tools](#) [Portals](#) [Download](#) [Submit](#) [News](#)

**Tools**

[Overview](#)  
[GO Term Enrichment](#)  
[JBrowse](#)   
[JBrowse2](#)   
[PhyloGenes](#)   
[GBrowse](#)   
[Synteny Viewer](#)   
[SeqViewer](#)   
[MapView](#)   
[Functional Categorization](#)   
[AraCyc Metabolic Pathways](#)  
[Integrated Genome Browser](#)  
[BLAST](#)   
[Patmatch](#)   
[Motif Analysis](#)   
[Chromosome Map Tool](#)   
[Textpresso Full Text](#)

(subscribed)

Gene 🔍

[Gene](#)  
[Clone](#)  
[Keyword](#)  
[Protein](#)  
[Polymorphisms](#)  
[Ecotype](#)  
[Person or Lab](#)  
[Germplasm](#)  
[Marker](#)  
[Vector](#)  
[Transposon](#)

# TAIR subscription

Sinica has institutional subscription (unlimited access)



Purchase usage units for individual academic or non-profit use [i](#)

## Subscription Benefits

- Unlimited access to TAIR for institutions
- Up-to-date, manually curated data from the literature
- Custom datasets on request
- Downloadable, current genome-wide datasets

## Choose License Type



Institutional  
Academic

Recommended



Individual  
Academic



Commercial

NEXT

## Individual Access Options

	Complimentary	Regular user	Frequent user
Usage units	50	300	900
Annual cost, per purchase	No purchase necessary	\$200 for first, \$500 for subsequent	\$1125
Visit frequency	A few times a year	Once a week	Every day
Average # of premium data detail pages visited (1 unit each/24 hr period)	About 20 a year	20 to 200 a year	300 to 400 a year
Average # of premium downloads (25 units each/24 hr period)	1 a year	2 to 4 a year	6 to 8 a year
Tool use (e.g., BLAST, JBrowse) (1 unit each/24 hr period)	Five or so times	20 to 50	100 to 200

# Search results and locus page

## TAIR Search Results

New Search Download All Download Checked

Get GO Annotations Get PO Annotations Get Sequences Get Gene Descriptions Get Locus History

Get Microarray Elements

Your query for genes where gene name, description, phenotype, locus name, uniprot id or GenBank accession contains the term **TFL1** resulted in **8** matches

Select All Clear Selected Displaying 1 - 8 of 8 results Results per page (top): 25 « < 1 > »

No.	Locus	Description ?
1	<input type="checkbox"/> <a href="#">AT5G03840</a>	Other Names: TERMINAL FLOWER 1;TFL-1;TFL1 Controls inflorescence meristem identity. Involved in the floral initiation process. Ortholog of the Antirrhinum gene CENTRORADIALIS (CEN). Involved in protein trafficking to the protein storage vacuole. TFL1 plays an antagonistic role to FT/TSF in the determination of inflorescence meristem identity.
2	<input type="checkbox"/> <a href="#">AT1G18100</a>	Other Names: E12A11;MFT;MOTHER OF FT AND TFL1 Encodes a member of the FT and TFL1 family of phosphatidylethanolamine-binding proteins. It is expressed in seeds and up-regulated in response to ABA. Loss of function mutants show decreased rate of germination in the presence of ABA. ABA dependent regulation is mediated by both ABI3 and ABI5. ABI5 promotes MFT expression primarily in the radicle-hypocotyl



## Locus: AT5G03840 (TFL1) Premium Page

### Summary

**Gene** protein\_coding  
**Model**  
**Type**

**Symbols** TFL1 (TERMINAL FLOWER 1) (Primary Symbol), TFL-1 (TERMINAL FLOWER 1)

### Description

Controls inflorescence meristem identity. Involved in the floral initiation process. Ortholog of the Antirrhinum gene CENTRORADIALIS (CEN). Involved in protein trafficking to the protein storage vacuole. TFL1 plays an antagonistic role to FT/TSF in the determination of inflorescence meristem identity.

### Community Comments

Add My Comment Show Comments

### Update History

No update history available

**Date last modified** 2022-01-27

**TAIR Accession** Locus:2150595

### Summary

### Transcripts

### Maps and Mapping Data

### Sequences

### Protein Data

### Expression

### Gene Ontology

### Homology

### Germplasm and Clones

### Polymorphisms

### Publications

### External Links

# Transcripts

representative gene model: In TAIR, this is the reference gene model for the locus.  
It's likely to be the most common and abundant form.



Locus: AT5G03840 (TFL1)  Premium Page

## Transcripts

Representative Gene Model [AT5G03840.1](#)

Different models can have different transcription start, end or splicing junction

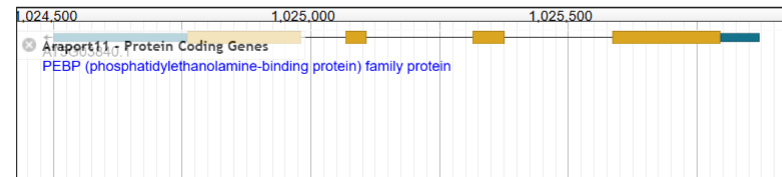
### Associated Transcripts

Type 	Transcript Count 
EST	(2)
cDNA	(2)

Associated Transposons No Associated Transposons found

## Maps and Mapping Data

Map Detail Image



[Center on AT5G03840](#) | [Full-screen view](#)

Link to Jbrowse

yellow box: coding exon; blue box: untranslated region (5' or 3' UTR); thin line: intron

# Genome browser

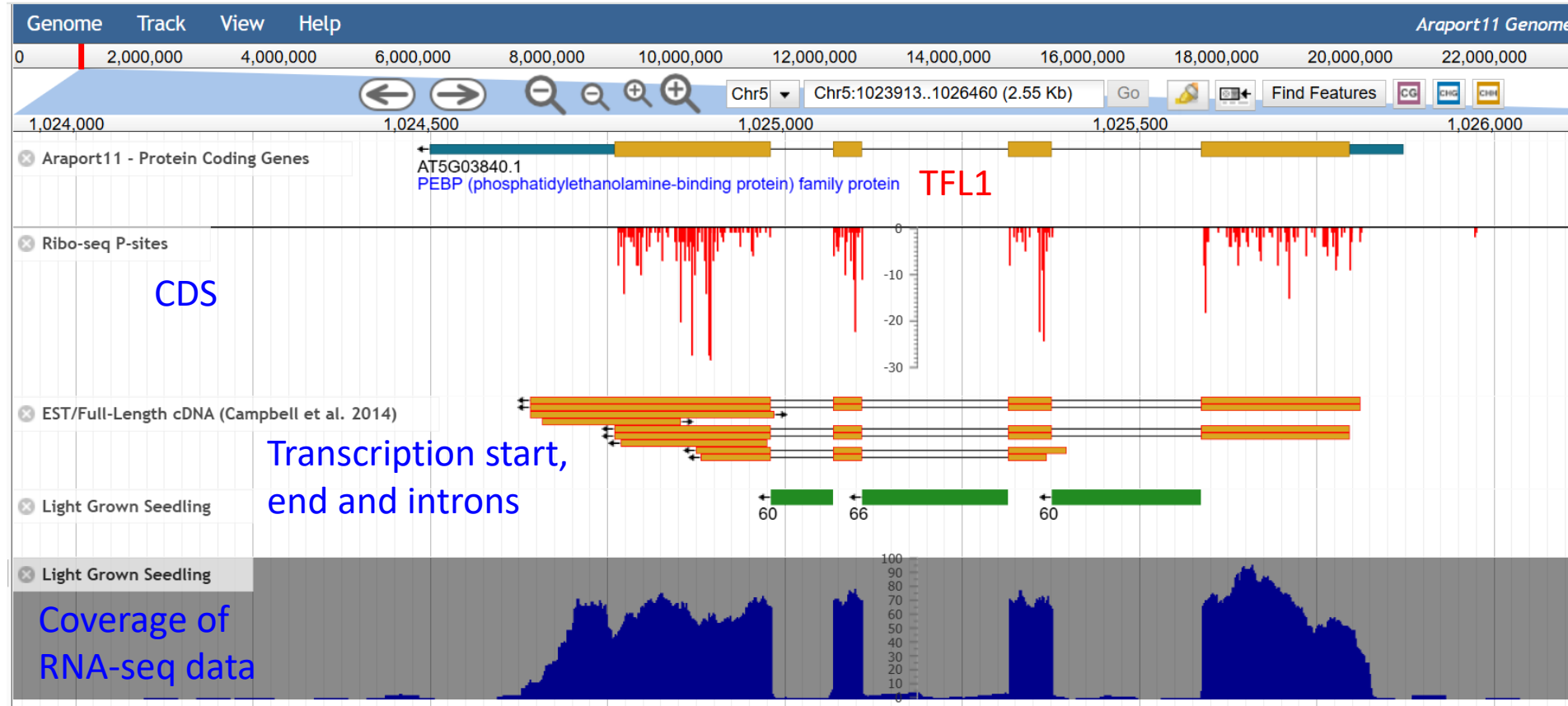
An important tool for users to visualize and browse entire genomes with annotated data or omic data, including gene structure, sequence variation, mutations, RNA-seq data, Ribo-seq data and peptide data etc.

Tracks Available in Faceted List	
CoGe EPIC-CoGe ▶	
▼ Community Data	104
▼ lncRNAs	1
<input type="checkbox"/> Arabidopsis lncRNAs	
▶ Stress induced TARs and Peptides	2
▶ Translated uORFs (TuORFs)	5
▶ Variation	7
▶ Proteomics	4
▶ Splicing	2
▶ UTR	4
▶ EST and Protein Alignments	3
▶ Repeat	3
▶ Microarray	1
▶ Genomic Elements	2
▶ Hypoxia Gene Regulation	40
▶ Cap Analysis of Gene Expression (CAGE)	9
▶ pENCODE	9
▶ TIF-seq, TSS-seq and plaNET-seq	12
▼ Arabidopsis Genome Assemblies	62
▼ Araport11	52
▶ Gene Structure Jun 2016   Symbols Oct 24	8
▼ RNA-seq based evidence	44
▶ Splice Junctions	11
▶ Transcript Assembly	11
▶ Mapping Coverage	11
▶ Aligned Reads	11

▼ Hypoxia Gene Regulation	40
▶ ATAC-Seq	10
▶ ChIP-Seq	17
▶ nRNA-Seq	5
▶ mRNA-Seq	5
▶ TRAP-Seq	3
▶ Cap Analysis of Gene Expression (CAGE)	9
▼ pENCODE	9
▼ SchmitzLab - Lu_Z et al, 2019, Nature Plants	9
▶ ATAC-seq	1
▶ ChIP-seq	6
▶ RNA-seq	1
▶ MethylC-seq	1
▼ TIF-seq, TSS-seq and plaNET-seq	12
<input type="checkbox"/> TSS-seq Cold_3hr (Kindgren et al. 2018)	
<input type="checkbox"/> TSS-seq hen2 (Kindgren et al. 2020)	
<input type="checkbox"/> TSS-seq spt16 (Nielsen et al. 2019)	
<input type="checkbox"/> TSS-seq ssrp1 (Nielsen et al. 2019)	
<input type="checkbox"/> TSS-Seq WT (Nielsen et al. 2019)	
<input type="checkbox"/> plaNET-seq Cold_12hr (Kindgren et al. 2020)	
<input type="checkbox"/> plaNET-seq Cold_3hr (Kindgren et al. 2020)	
<input type="checkbox"/> plaNET-seq DMSO (Kindgren et al. 2020)	
<input type="checkbox"/> plaNET-seq DMSO+PlaB (Kindgren et al. 2020)	
<input type="checkbox"/> plaNET-seq untreated (Kindgren et al. 2020)	
<input type="checkbox"/> TIF-Seq WT (Thomas et al. 2020)	
<input type="checkbox"/> TIF-Seq hen2 (Thomas et al. 2020)	

# Genome browser: Jbrowse

Check the accuracy of gene model (transcription start, end, introns, and CDS)



Do you agree with this model? If not, what changes will you make?



# Genome browser: sequence variation among ecotypes

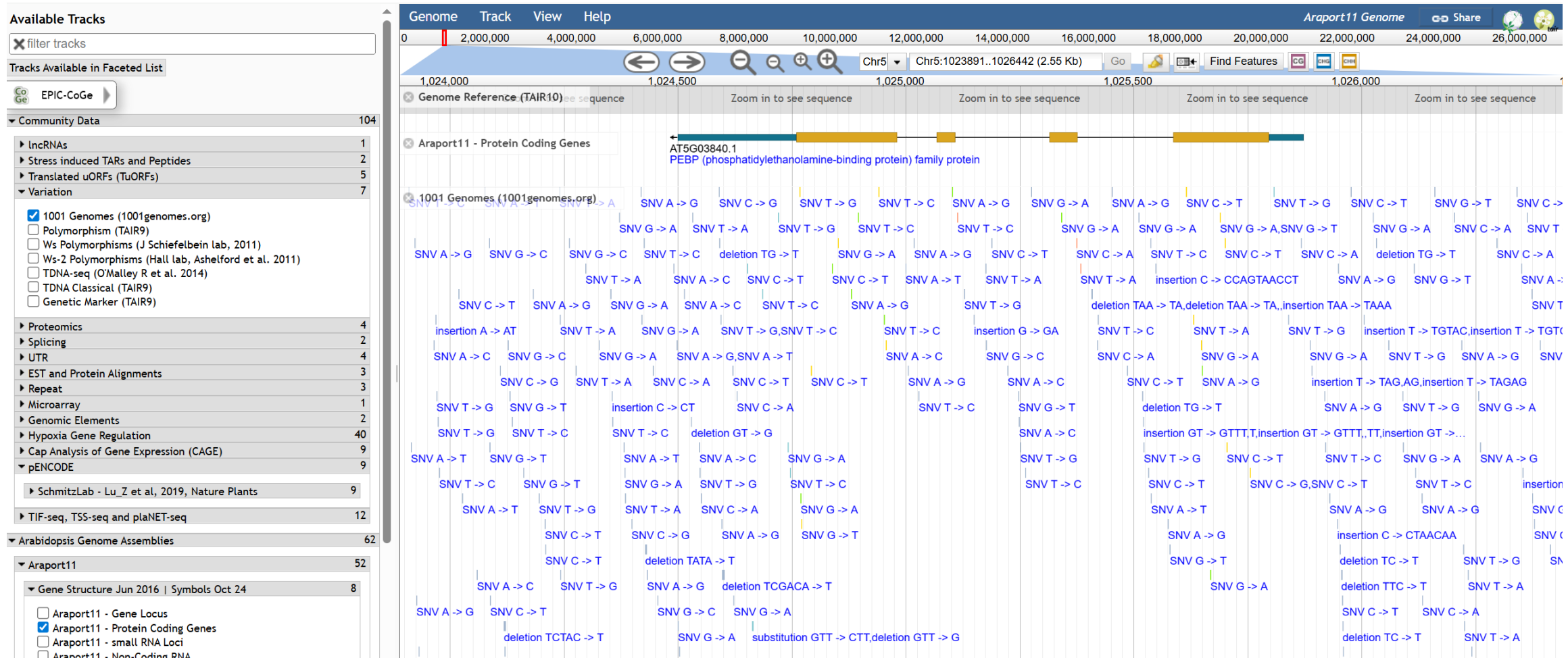
reference genome  $\neq$  your genome

Col-0  
Ler  
Ws  
Cvi

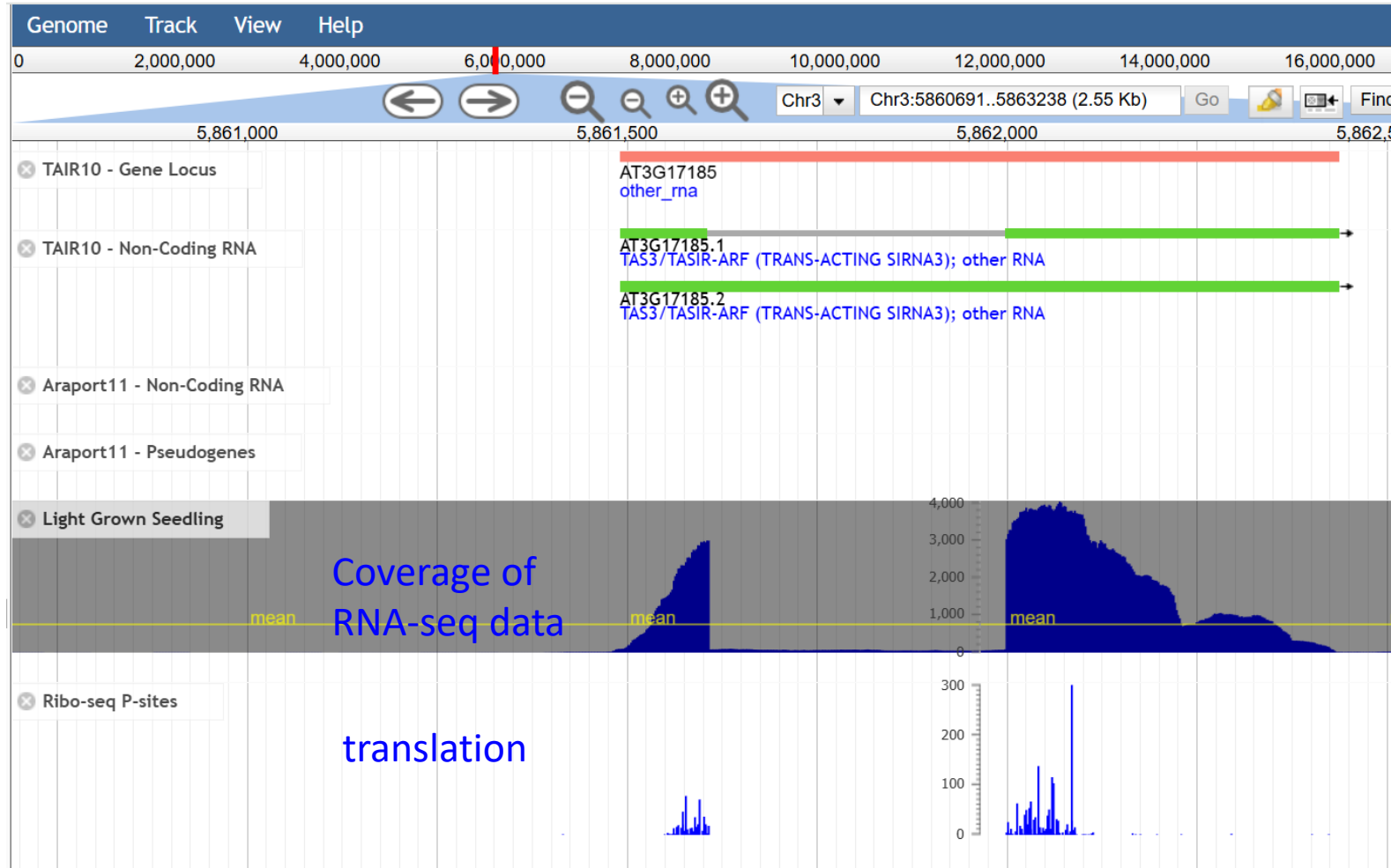
..

..

..



# Genome browser: hidden RNA or open reading frame



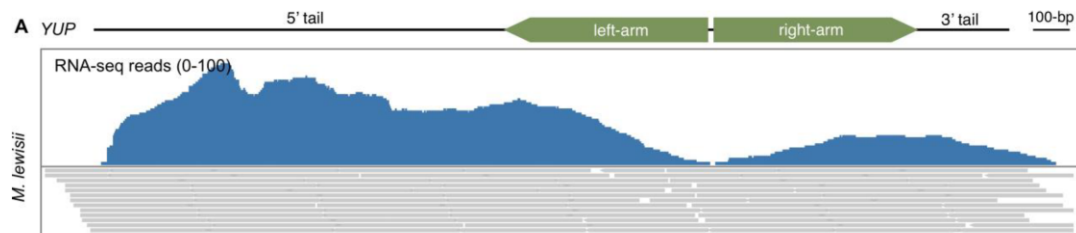
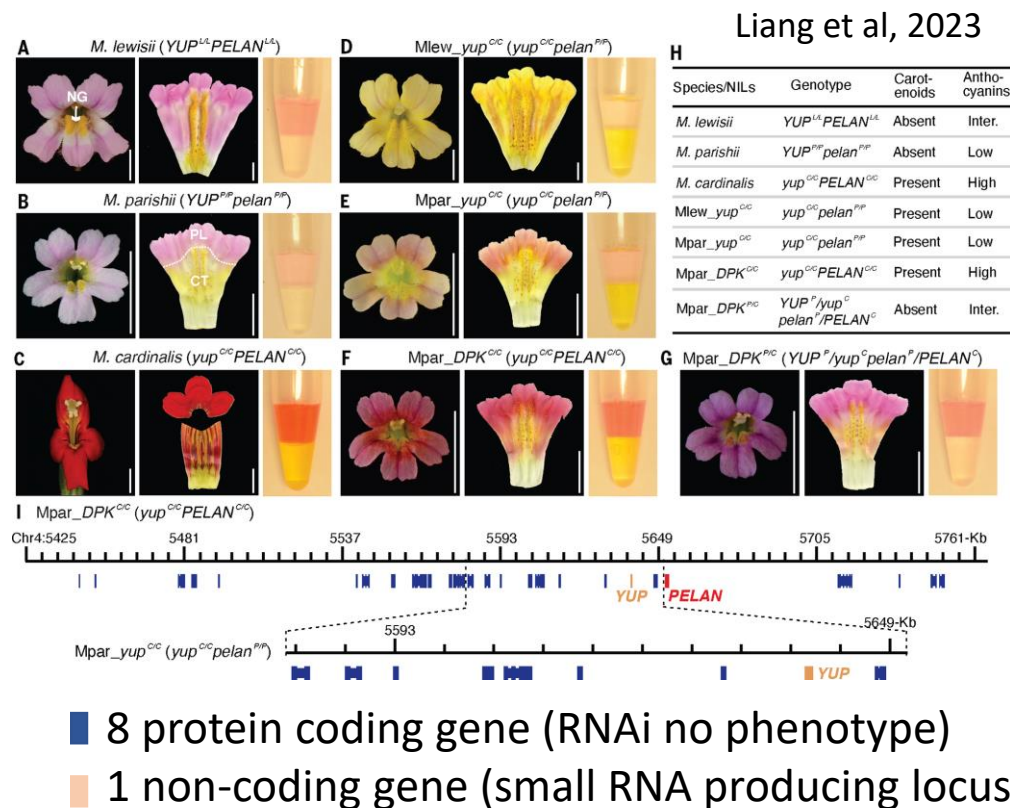
# Genome browser: non-coding RNA in monkey flower

“Unusual suspects in flower color evolution”



Science 2023

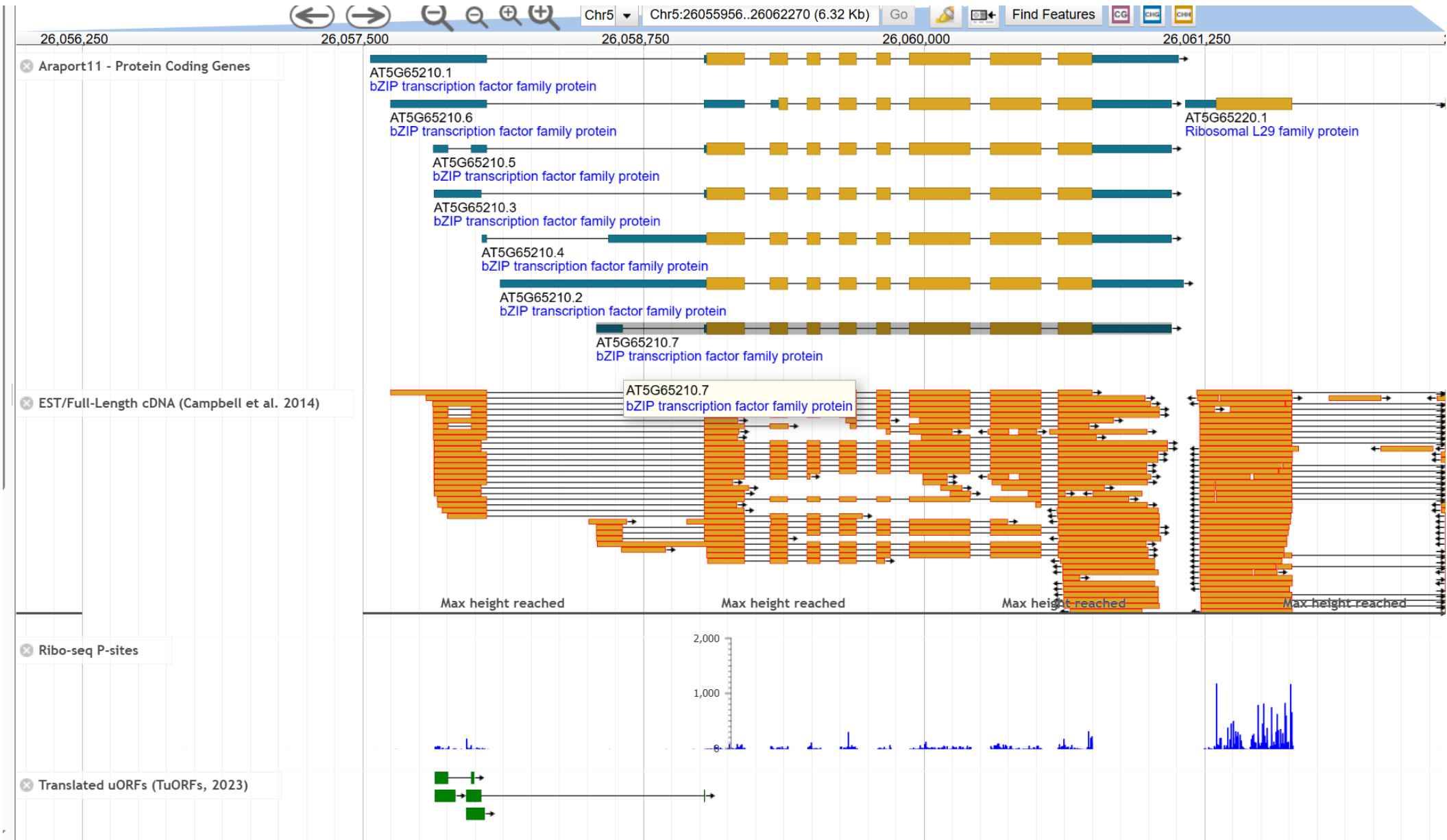
*YUP*: yellow carotenoid pigments in the petal upper epidermis



# Exercise I

## **TGA1 (AT5G65210)**

1. number of isoforms ? (the differences)
2. the representative form in Araport11? Do you agree (check JBrowse)? If not, your answer?
3. Are there any upstream open reading frames?



# Locus page: DNA and protein sequences

Intron  
5'UTR  
CDS  
3' UTR

5'UTR  
CDS  
3' UTR

CDS

Protein sequence of  
the representative  
form

## Sequences

Sequence

[full length genomic](#) [full length cDNA](#) [full length CDS](#) [protein](#)

## Protein Data

Protein Data

Name ↓↑	Length ↓↑	Molecular Weight ↓↑	Isoelectric Point ↓↑	INTERPRO domains ↓↑
<a href="#">AT5G03840.1</a>	177	20158.1	10.29	<a href="#">PEBP_euk:IPR035810</a>

- Some gene models don't have 5' UTR or 3' UTR
- Some gene models have incorrect 5' UTR or 3' UTR
- If 5' UTR or 3' UTR is important to you, compare the annotation with ESTs/full length cDNA or RNA-Seq data in JBrowse



# Locus page: Expression

**BAR eFP Browser**

Data Source: **Developmental\_Map**

At5g03840

- Abiotic Stress II
- Abiotic Stress
- Biotic Stress II
- Biotic Stress
- Chemical
- Developmental\_Map**
- Developmental\_Mutants
- Development\_RMA
- Germination
- Guard\_Cell
- Hormone
- Klepikova\_Atlas
- Lateral\_Root\_Initiation
- Light\_Series
- Natural\_Variation
- Regeneration
- Root\_II
- Root
- Seed
- Shoot\_Apex

Cauli

Locus: AT5G03840 (TFL1) Premium Page

## Expression

Plant Ontology Annotations **20 unique annotations**

[View Annotation Details](#)

Category ↓↑	Relationship Type	Keyword ↓↑
Growth and Developmental Stages	expressed during	<a href="#">mature plant embryo stage</a> <a href="#">petal differentiation and expansion stage</a> <a href="#">plant embryo bilateral stage</a> <a href="#">plant embryo cotyledonary stage</a> <a href="#">plant embryo globular stage</a> <a href="#">vascular leaf senescent stage</a>
Plant structure	expressed in	<a href="#">collective leaf structure</a> <a href="#">flower</a> <a href="#">flower meristem</a> <a href="#">hypocotyl</a> <a href="#">inflorescence meristem</a> <a href="#">leaf apex</a> <a href="#">plant embryo</a> <a href="#">plant sperm cell</a> <a href="#">root</a> <a href="#">seed</a> <a href="#">shoot apex</a> <a href="#">vascular leaf</a>
Plant structure	located in	<a href="#">flower meristem</a> <a href="#">shoot system meristem</a>

**BAR eFP Browser**

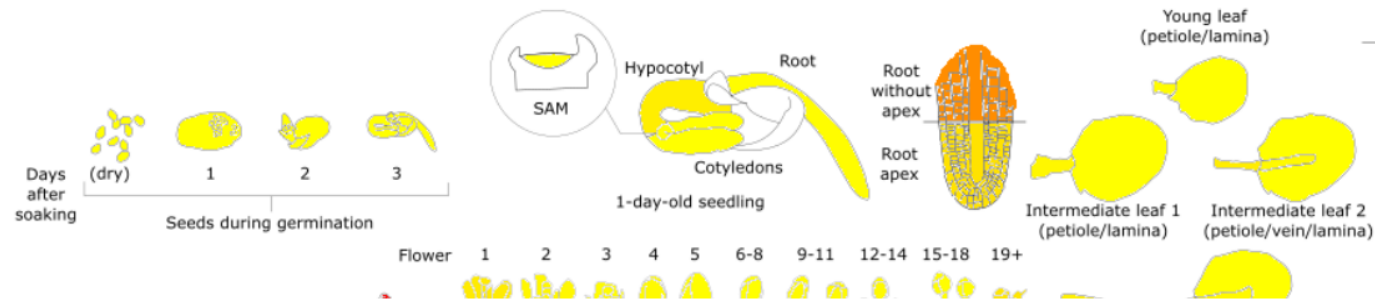
Data Source: **Klepikova\_Atlas**

AT5G03840

## Microarray, RNA-seq, single cell

Klepikova Arabidopsis Atlas eFP Browser at bar.utoronto.ca

Klepikova et al. 2016. Plant J. 88:1058-1070



# Development map expression

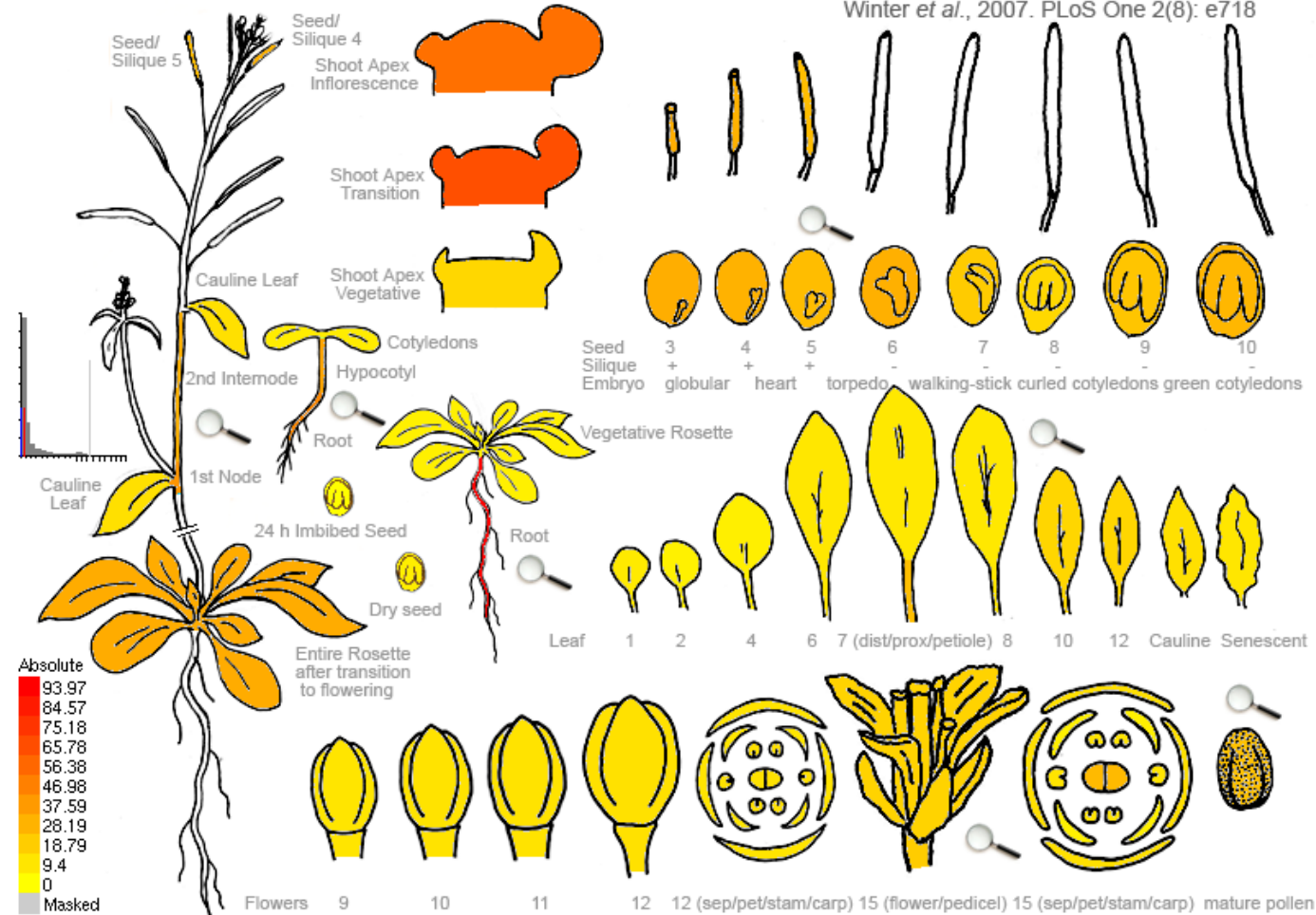
## BAR eFP Browser

Data Source

At5g03840 250869\_at

Arabidopsis eFP Browser at bar.utoronto.ca

Winter et al., 2007. PLoS One 2(8): e718



eFP Browser by B. Vinegar, drawn by J. Alls and N. Provart. Data from Gene Expression Map of Arabidopsis Development: Schmid et al., 2005, Nat. Gen. 37:501, and the Nambara lab for the imbibed and dry seed stages. Data are normalized by the GCOS method, TGT value of 100. Most tissues were sampled in triplicate.

# Single cell expression

BAR eFP Browser

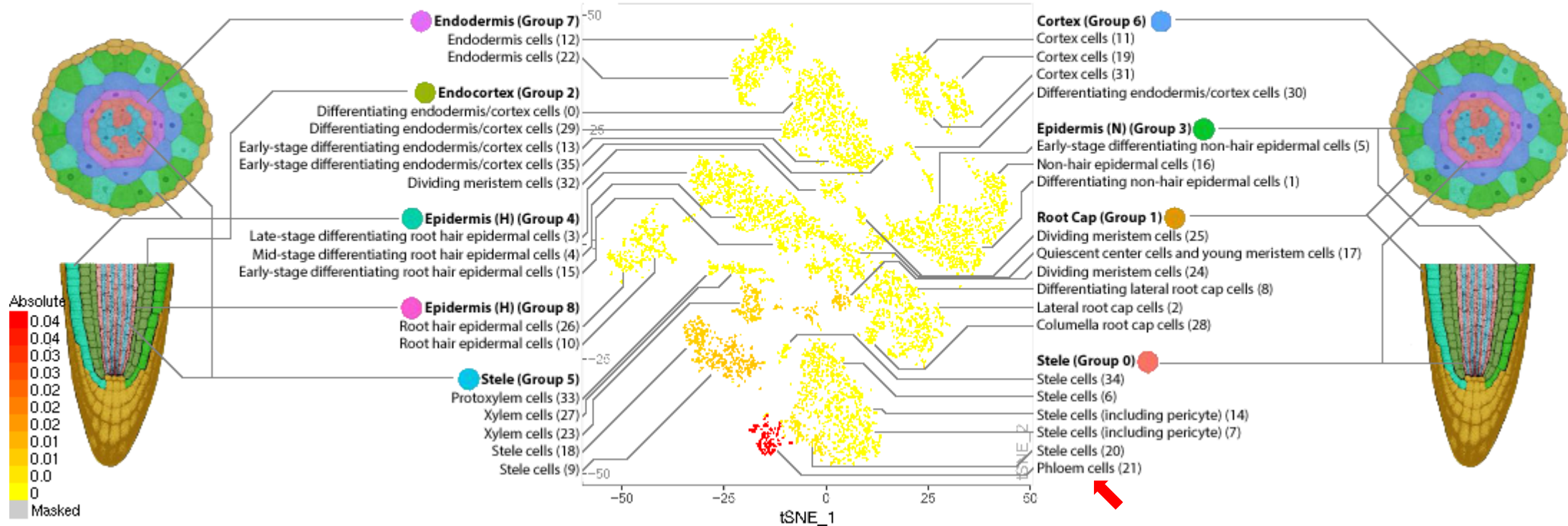
Data Source

AT5G03840

Root

scRNA-Seq at bar.utoronto.ca

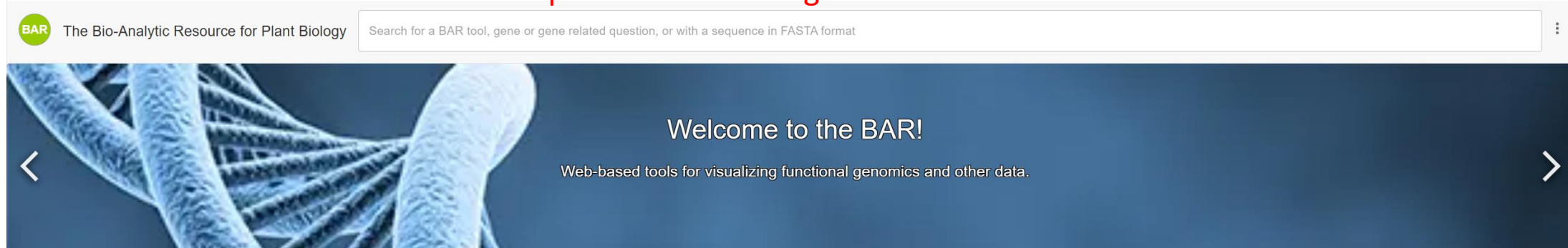
Ryu et al., Plant Physiology, DOI: 10.1104/pp.18.01482



# BAR: The Bio-Analytic Resource for plant biology

<https://bar.utoronto.ca/#OtherGenomicTools>

## Expression data and genomic tools



### Gene Expression and Protein Tools

View expression patterns as electronic fluorescent pictographs or heatmaps, explore promoters, identify protein-protein interactions and more.



### Molecular Markers and Mapping Tools

Perform Next Generation Mapping, or generate your own markers using our molecular marker tools.












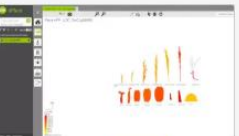








### Other Genomic Tools and Widgets

Remove duplicates, perform multi-dimensional Venn analyses, or generate random lists of identifiers.

# BAR: Gene expression in crops and other plants

ePlants

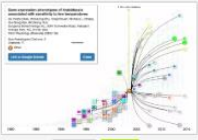
<b>ePlant</b>  Info Go Pub	<b>ePlant Maize</b>  Info Go	<b>ePlant Poplar</b>  Info Go	<b>ePlant Tomato</b>  Info Go	<b>ePlant Camelina</b>  Info Go	<b>ePlant Soybean</b>  Info Go
<b>ePlant Potato</b>  Info Go	<b>ePlant Barley V3</b>  Info Go	<b>ePlant Barley V1</b>  Info Go	<b>ePlant Medicago</b>  Info Go	<b>ePlant Eucalyptus</b>  Info Go	<b>ePlant Rice</b>  Info Go
<b>ePlant Willow</b>  Info Go	<b>ePlant Sunflower</b>  Info Go	<b>ePlant Cannabis</b>  Info Go	<b>ePlant Wheat</b>  Info Go	<b>ePlant Sugarcane</b>  Info Go	<b>Legacy ePlant (PLOS ONE version)</b>  Info Go Pub




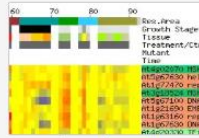
# BAR: Tools and widgets


## Other Genomic Tools and Widgets


Remove duplicates, perform multi-dimensional Venn analyses, or generate random lists of identifiers.

**Arabidopsis Citation Network Viewer**  
  
Info Go

**ClustalW with MView Output**  
  
Info Go

**DataMetaFormatter**  
  
Info Go

**Heatmapper**  
  
Info Go

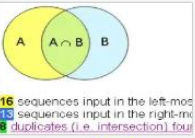
**Heatmapper Plus**  
  
Info Go

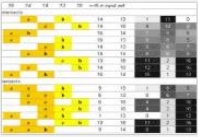
**Duplicate Remover**  

5 of the above had duplicate entries, listed below

A5g51210	(2 instances)
A5g53410	(2 instances)
A5g53310	(2 instances)
A5g54140	(2 instances)
A5g57300	(2 instances)

  
Info Go

**Venn Selector**  
  
Info Go


**Venn SuperSelector**  
  
Info Go

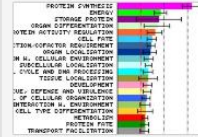
**Random ID list generator**  

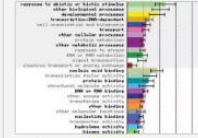
random\_list\_1 random\_list\_2 random\_list\_3

AT3G20570	AT1G29795	AT4G3598
AT2G29500	AT4G27360	AT4G3360
AT3G00740	AT5G52000	AT3G3390
AT2G30210	AT1G10500	AT2G2211
AT1G00500	AT1G03070	AT2G2744
AT3G44295	AT4G13700	AT4G2085
AT5G10230	AT5G19730	AT1G2644
AT2G24570	AT3G45810	AT2G3228
AT5G38770	AT3G43610	AT5G0222
AT4G00230	AT4G10372	AT3G2779
AT5G08630	AT1G74230	AT1G08611

  
Info Go

**AGURR**  
  
Info Go

**Classification Super Viewer**  
  
Info Go Pub

**Medicago Classification Super Viewer**  
  
Info Go Pub


**\_at to AGI converter**  

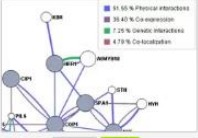
At1g54100.263157_at	ALDH7B4__ald induced gene 2
At1g76750.252947_at	CASA1, GASA4 g:807930 gb.U1
At2g15970.265490_at	COR413-PM1, g:18449102 gb cold acclimat
At2g26990.357612_at	g:18449102 gb cold acclimat
At1g17745.255403_at	PGDH__D-3-ph
At2g47770.386462_at	benzodiazepine
At1g55580.300806_at	GUS2_3__hydrol


  
Info Go


**MASTA**  


Overlap search with C1581PNO0\_3h


  
Info Go

**GeneMANIA**  
  
Info Go

**Topo-phylogeny**  
  
Info Go Pub

**BAR API**  
  
Info Go

**Custom eFP Creator**  
  
Info Go

**Downloads**  
  
Info Go



# Gene ontology (GO)

Gene Ontology		
21 unique annotations		
<a href="#">View Annotation Details</a>		
Category ↕	Relationship Type ↕	Keyword ↕
GO Biological Process	acts upstream of or within	<a href="#">meristem determinacy</a> <a href="#">negative regulation of flower development</a> <a href="#">protein targeting to vacuole</a> <a href="#">response to sucrose</a>
GO Biological Process	involved in	<a href="#">negative regulation of flower development</a> <a href="#">vegetative to reproductive phase transition of meristem</a>
GO Cellular Component	is active in	<a href="#">cytoplasm</a> <a href="#">nucleus</a>
GO Cellular Component	located in	<a href="#">cytoplasm</a> <a href="#">nucleus</a> <a href="#">plasma membrane</a> <a href="#">vacuole</a> <a href="#">vesicle</a>
GO Molecular Function	enables	<a href="#">transcription coregulator activity</a>

Functional annotations with [controlled vocabulary](#) terms :

**Gene Ontology (GO)**

[Genes function](#) and [localization](#) of the gene product.

Most gene annotations are made by curators using the [published literature](#) as sources. Some annotations are based on [computational methods](#). Detailed information including references and supporting evidence can be obtained by clicking on the link to view Annotation Detail.

# Annotation details

Select All


Clear Selected

Displaying 1 - 23 of 23 results

Results per page (top): 25

No.	Locus	Gene Model	Gene Symbol/Full Name	Relationship Type	Keyword	Keyword Category	Evidence:Description:With	Reference
1	<input type="checkbox"/>	<a href="#">AT5G03840.1</a>		located in	<a href="#">cytoplasm</a>	cellular component	<i>inferred from sequence model:</i> predicted protein features:	<a href="#">AtSubP analysis</a> <b>prediction</b>
2	<input type="checkbox"/>	<a href="#">AT5G03840</a>	TFL1/TERMINAL FLOWER 1	acts upstream of or within	<a href="#">response to sucrose</a>	biological process	<i>inferred from mutant phenotype:</i> mutant growth experiment with supplementation of substrates: NONE	<a href="#">Ohto et al (2001)</a>
3	<input type="checkbox"/>	<a href="#">AT5G03840</a>	TFL1/TERMINAL FLOWER 1	acts upstream of or within	<a href="#">negative regulation of flower development</a>	biological process	<i>inferred from mutant phenotype:</i> analysis of physiological response: NONE	<a href="#">Shannon et al (1991)</a>
4	<input type="checkbox"/>	<a href="#">AT5G03840</a>	TFL1/TERMINAL FLOWER 1	acts upstream of or within	<a href="#">protein targeting to vacuole</a>	biological process	<i>inferred from mutant phenotype:</i> biochemical/chemical analysis: NONE	<a href="#">Sohn et al (2007)</a>
5	<input type="checkbox"/>	<a href="#">AT5G03840</a>	TFL1/TERMINAL FLOWER 1	involved in	<a href="#">vegetative to reproductive phase transition of meristem</a>	biological process	<i>Inferred from Biological aspect of Ancestor:</i> none: PANTHER:PTN002260847 TAIR:locus:2038643	<a href="#">Annotation inferences using phylogenetic trees</a> <b>prediction</b>

# Using GO to identify genes with similar functions

Summary		
🔍 Name	negative regulation of flower development	
🔍 Synonyms	inhibition of flower development,down-regulation of flower development,down regulation of flower development,downregulation of flower development	
Date Last Modified	2010-11-18	
Definition	Any process that stops, prevents, or reduces the frequency, rate or extent of flower development.	
🔍 External ID	<a href="#">GO:0009910</a>	
Keyword Category	biological process	
🔍 Data Associated To This Term		
Publications 	Annotations 	Loci 
<a href="#">43</a>	<a href="#">62</a>	<a href="#">50</a>
🔍 Data Associated To Children Terms	No data associated to this term.	
🔍 TreeView	<a href="#">Keyword TreeViewer</a>	

<a href="#">Select All</a> <a href="#">Clear Selected</a>		Displaying 1 - 25 of 50 results	
No.	Locus	Description ?	
1	<input type="checkbox"/> <a href="#">AT2G27550</a>	Other Names: ATC;centroradialis encodes a protein similar to TFL1. overexpression leads to similar phenotype as TFL1 overexpression. expressed specifically in the hypocotyl	
2	<input type="checkbox"/> <a href="#">AT5G65060</a>	Other Names: AGAMOUS-LIKE 70;AGL70;FCL3;MADS AFFECTING FLOWERING 3;MAF3 MADS domain protein - flowering regulator that is closely related to FLC	
3	<input type="checkbox"/> <a href="#">AT5G65070</a>	Other Names: AGAMOUS-like 69;AGL69;FCL4;MADS AFFECTING FLOWERING 4;MAF4	

# Finding crop orthologs

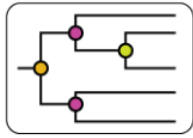
Locus: AT5G03840 (TFL1)  Premium Page

## Homology

Gene Families

[EnsemblPlants](#) [PhytoGenes](#) [InParanoid Ortholog Groups](#) [Phytozome](#) [PANTHER](#) [PLAZA](#)

Panther Tree Viewer



PHYLO  
GENES

View complete family and tree

PANTHER Plant Homologs

Arabidopsis paralogs ?

[AT1G18100 \(MFT\)](#)

[AT1G65480 \(FT\)](#)


[Show More ...](#)

Organism	UniProt ID	Gene ID	Ortholog Type	
Amborella trichopoda	W1NUA1	AMTR_s00114p00070400	LDO	
Brachypodium distachyon (purple false brome)		I1IA72	BRADI_3g44860v3	0
Brachypodium distachyon (purple false brome)		I1IUB1	BRADI_4g42400v3	0
Brachypodium distachyon (purple false brome)		I1IXH1	BRADI_5g09270v3	LDO
Brassica napus (rapeseed)	O82152	GSBRNA2T00073025001	O	
Brassica napus (rapeseed)	A0A078FPC4	GSBRNA2T00078727001	O	
Brassica rapa (Chinese cabbage)	M4CNJ5	Bra005783	LDO	
Brassica rapa (Chinese cabbage)	M4CZ61	Bra009508	O	
Brassica rapa (Chinese cabbage)	M4EJ50	Bra028815	O	
Capsicum annuum (pepper)	A0A1U8EDW2	T459_22372	LDO	
Citrus sinensis (orange)	A0A067F1A2	CISIN_1g035977mg	LDO	
Cucumis sativus (cucumber)	B9ZYL2	Csa_3G776350	LDO	

Get Sequences

Download AGI IDs

Plant orthologs ?

Download Orthologs 

### Eudicotyledons

Brassica napus  
Brassica rapa  
Capsicum annuum  
Citrus sinensis  
Cucumis sativus  
Erythranthe guttata  
Eucalyptus grandis  
Glycine max  
Gossypium hirsutum  
Juglans regia  
Manihot esculenta  
Medicago truncatula  
Nicotiana tabacum

2  
3  
1  
1  
2  
1  
1  
4  
3  
2  
3  
2  
4



### Monocotyledons

Brachypodium distachyon  
Hordeum vulgare  
Musa acuminata  
Oryza sativa  
Setaria italica  
Sorghum bicolor  
Triticum aestivum  
Zea mays  
Zostera marina

3  
3  
5  
4  
4  
4  
8  
6  
1

### Other plants


Amborella trichopoda  
Klebsormidium nitens  
Marchantia polymorpha

1  
5  
2

# Finding orthologs with Blast search

## Sequences













Sequence [full length genomic](#) [full length cDNA](#) [full length CDS](#) [protein](#)



Home | Help | Contact


Enter search text

Advanced Search ▾ | Browse ▾ | Tools ▾

- Overview
- GO Term Enrichment
- JBrowse 
- JBrowse2 
- PhyloGenes 
- GBrowse 
- Synteny Viewer 
- SeqViewer 
- MapView 
- Functional Categorization 
- AraCyc Metabolic Pathways
- Integrated Genome Browser
- BLAST  ←**
- Patmatch 
- Motif Analysis 
- Chromosome Map Tool 
- Textpresso Full Text

NCBI <https://blast.ncbi.nlm.nih.gov/Blast.cgi>


Web BLAST



**Nucleotide BLAST**  
nucleotide ► nucleotide

**blastx**  
translated nucleotide ► protein

**tblastn**  
protein ► translated nucleotide



**Protein BLAST**  
protein ► protein

- search homologs
- map transcripts
- examine the specificity of primers
- .....

# Blast : homolog search

Protein search is more sensitive than nucleotide search  
Use BLASTP or BLASTX for searching homologs

TAIR BLAST 2.9.0+ 

This form uses [NCBI BLAST 2.9.0+](#)  
View help documentation [here](#)

**Blast**

BLAST™ program:

Datasets:

Input Type:

Input:

Choose a file:

Raw, FASTA, GCG and RSF formats accepted.

☒ Filter Query

BLASTN: NT query, NT db

Select your option

BLASTN: NT query, NT db

BLASTP: AA query, AA db

BLASTX: NT query, AA db

TBLASTN: AA query, NT db

TBLASTX: NT query, NT db (All 6 Frames)

Choose File

No file chosen

+

Advanced BLAST™ Parameter Options





# Blast search: short sequences (e.g. primers)

Advanced BLAST™ Parameter Options

Weight Matrix:	
Max Scores:	100
Max Alignments:	50
Gapped Alignments:	Yes
Expectation:	10
Nucleic Mismatch:	-3
Nucleic Match:	2
Gap Opening Penalty:	0 (use default)
Gap Extension Penalty:	0 (use default)
Extension Threshold:	0 (use default)
Word Size:	0 (use default)
Query and Database Genetic Code:	Standard or Universal (default)

Increase to 100 if query sequence is short (<20 nt) and expect imperfect hits

11->7 (for short query)



**Important update**

The *ClusteredNR* database is now the **default** Protein BLAST database. [Learn more about ClusteredNR](#)

**Standard Nucleotide BLAST**

**blastn**

blastp

blastx

tblastn

tblastx

BLASTN programs search nucleotide databases using a nucleotide query. [more...](#)

**Enter Query Sequence**

Enter accession number(s), gi(s), or FASTA sequence(s) [?](#) [Clear](#)

Query subrange [?](#)

From

To

Or, upload file

選擇檔案 未選擇任何檔案 [?](#)

Job Title

Enter a descriptive title for your BLAST search [?](#)

☐ Align two or more sequences [?](#)

**Program Selection**

Optimize for

- ☒ Highly similar sequences (megablast)  
☐ More dissimilar sequences (discontiguous megablast)  
☐ Somewhat similar sequences (blastn) ← **Short query sequence (e.g. primer)**

Choose a BLAST algorithm [?](#)

Megablast is intended for comparing a query to closely related sequences and works best if the target percent identity is 95% or more but is very fast.


Discontiguous megablast uses an initial seed that ignores some bases (allowing mismatches) and is intended for cross-species comparisons.

BlastN is slow, but allows a word-size down to seven bases.

[more...](#)

# Mutants and phenotypes

Locus: AT5G03840 (TFL1)  Premium Page

 Germplasms 15 / 20 entries

[View Complete List](#)

[Search ABRC](#)

[Search RIKEN](#)

[Search NASC](#)

Name

[CS6167](#)

Polymorphisms

[gl1-3](#); [tfl1-1](#)

Background

Phenotypes

Phenotype curated by ABRC.

- early flowering; **determinate inflorescence** with terminal compound floral structure consisting of 2 or 3, sometimes incomplete, flowers; more severe phenotype at higher temperatures and longer photoperiods; lacks trichomes on stems and leaves.

Images



Name

[CS6235](#)

Polymorphisms

[tfl1-11](#)

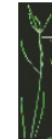
Background

Phenotypes

Phenotype curated by ABRC.

- strong allele, early flowering, reduced plant height and increased number of rosette inflorescences; determinate inflorescences; terminal region of primary inflorescence may consist of a single flower or of 2-3 clustered flowers separated by short internodes, in which organs of the 3 outer whorls are missing or are mosaic; secondary inflorescence apices are determinate and usually converted into a single normal flower; 2-5 normal flowers/inflorescence; photoperiod affects phenotype.

Images



Name

[CS6237](#)

Polymorphisms

[tfl1-13](#)

Background

Phenotypes

Phenotype curated by ABRC.

- strong allele; early flowering; **reduced plant height**; increased number of rosette inflorescences, determinate inflorescences; terminal region of primary inflorescence may consist of a single flower or of 2-3 clustered flowers separated by short internodes, in which the organs in the 3 outer whorls are missing or are mosaic; secondary inflorescence apices are determinate and usually converted into a single normal flower; 2-5 normal flowers/inflorescence; photoperiod affects phenotype.


Images



Test your hypothesis using Arabidopsis mutants

# Mutant order through ABRC (not our ABRC)

Need to apply an account for making order

Polymorphism: tf11-2  Premium Page

---

### Summary


Name	tf11-2
Date Last Modified	2007-05-22
Aliases	None available
Tair Accession	Polymorphism: 4770445


### Germplasms


? Germplasm





[Search at ABRC](#) [Search at NASC](#)

Name	Polymorphisms
<a href="#">CS3091</a>	tf11-2

 **ABRC** ARABIDOPSIS BIOLOGICAL RESOURCE CENTER

 **GIVE**

 **THE OHIO STATE UNIVERSITY**

PLEASE SUPPORT ABRC: Donate your seed and other resources. We are currently interested in receiving characterized mutants, especially new CRISPR mutants. Financial donations are also welcomed through the "GIVE" link above.

You are already signed in.

## Name / Stock Number: CS3091

donor stock number: tf11-2

NASC stock number: [N3091](#)

Resource Type: seed

Availability: available

## Description:

mutant

Growth Requirement: none


Marker:


[View Order History](#)


[Add To Cart](#)

**See who has ordered this mutant**

# Stock order histories

 **ABRC** ARABIDOPSIS BIOLOGICAL RESOURCE CENTER





PLEASE SUPPORT ABRC: Donate your seed and other resources. We are currently interested in receiving mutants. Financial donations are also welcomed through the "GIVE" link above.

Signed in successfully.

Search for Stock Number:

CS3091

Order Date

To:

From:

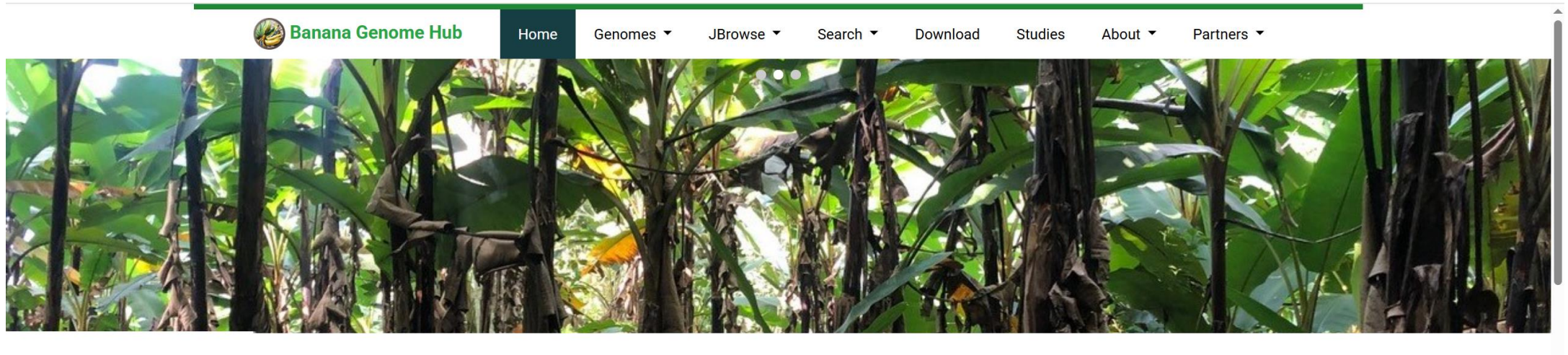
Search Orders

Order Date	Order Number	Ordered By	PI
2023-11-01	149262	Barry Pogson	Barry Pogson
2023-06-29	143925	Barry Pogson	Barry Pogson

2013-11-05	T104218	Chung-Mo Park	Chung-Mo Park
2013-08-16	T102573	Ariel Orellana	Ariel Orellana
2013-04-05	T99460	Vi Nguyen	Yuhai Cui
2013-03-21	T99143	Zheng Wang	Zhixi Tian
2012-12-19	T97305	Ying Wang	Paula Pijut
2012-11-14	T96529	Huazhong Ren	Huazhong Ren
2012-09-27	T95467	Hidetoshi Ikegami	Hidetoshi Ikegami
2012-05-27	T92681	Bin Liu	Bin Liu
2012-05-15	T92386	Tien-Shin Yu	Tien-Shin Yu
2012-04-11	T91510	Byeong-ha Lee	Byeong-ha Lee

# Banana genome

- Banana: AA, AAA, BB, AAB, AAAB genome
- Triploid banana: sterile
- A reference A genome (DH Pahang): 2012 (v1); 2021 Telomere-to-telomere (v4)
- AAA Cavendish: 2023





# Mapping genes in crops

Identify candidate genes responsible for a trait

- e.g. Disease resistance

PC



mutations



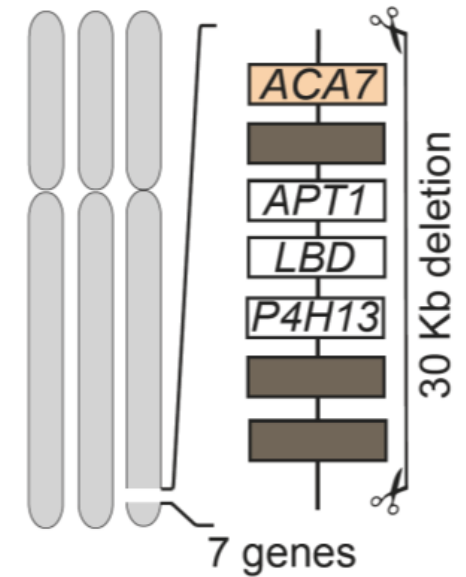
?

TC5



Hypothesis:  
A negative regulator of  
plant immunity

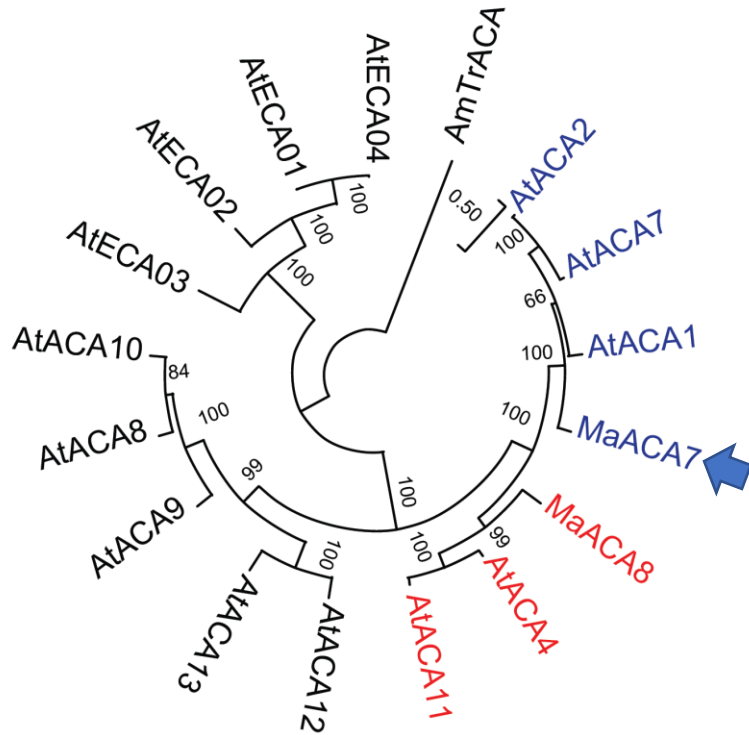
TC5 chr04



# Finding Arabidopsis orthologs

1. BLAST banana protein against TAIR protein database
2. Identify orthologs
3. Check the functions Arabidopsis orthologs

B



Locus: AT1G27770 (ACA1) Premium Page

## Summary

Gene Model Type	protein_coding
Symbols	ACA1 (autoinhibited Ca <sup>2+</sup> -ATPase 1) (Primary Symbol), PEA1 (PLASTID ENVELOPE ATPASE 1)
Description	Encodes a chloroplast envelope Ca <sup>2+</sup> -ATPase with an N-terminal autoinhibitor.

## Gene Ontology



28 unique annotations

[View Annotation Details](#)

Category	Relationship Type	Keyword
GO Biological Process	involved in	<a href="#">calcium ion transmembrane transport</a>
GO Cellular Component	is active in	<a href="#">intracellular membrane-bounded organelle</a> <a href="#">plasma membrane</a>
GO Cellular Component	located in	<a href="#">chloroplast</a> <a href="#">chloroplast inner membrane</a> <a href="#">endoplasmic reticulum</a> <a href="#">nucleus</a>
GO Molecular Function	enables	<a href="#">P-type calcium transporter activity</a> <a href="#">calcium channel activity</a> <a href="#">calmodulin binding</a>

# Functions of Arabidopsis orthologs

- Annotations could be incomplete or incorrect
- Read key papers

Publications			
15 / 15 entries		Results per page: 10	
Author/Title ↑↓	Source ↑↓	Associated Loci ↑↓	Date ↑↓
<a href="#">Wang, S., Zhang, C., Chen, R. et al.</a> H2S is involved in drought-mediated stomatal closure through PLD?1 in Arabidopsis	PLANTA	<a href="#">AT1G12480</a> ; <a href="#">AT1G27770</a> ; <a href="#">AT2G13610</a> ; <a href="#">AT2G26770</a> ; <a href="#">AT2G38170</a> ; <a href="#">AT3G15730</a> ; <a href="#">AT3G52720</a> ; <a href="#">AT3G62130</a> ; <a href="#">AT4G33950</a>	2024
<a href="#">Kramer, M. C., Kim, H. J., Palos, K. R. et al.</a> A Conserved Long Intergenic Non-coding RNA Containing snoRNA Sequences, IncCOBRA1, Affects Arabidopsis Germination and Development	FRONT PLANT SCI	<a href="#">AT1G05907</a> ; <a href="#">AT1G05913</a> ; <a href="#">AT1G05917</a> ; <a href="#">AT1G18080</a> ; <a href="#">AT1G27770</a> ; <a href="#">AT3G03415</a> ; <a href="#">AT3G03425</a> ; <a href="#">AT3G03445</a> ; <a href="#">AT3G05655</a>	2022
 <a href="#">Rahmati Ishka, M., Brown, E., Rosenberg, A. et al.</a> Arabidopsis Ca2+-ATPases 1, 2, and 7 in the endoplasmic reticulum contribute to growth and pollen fitness	PLANT PHYSIOLOGY	 <a href="#">AT1G27770</a> ; <a href="#">AT2G14610</a> ; <a href="#">AT2G41560</a> ; <a href="#">AT3G57260</a>	2021
<a href="#">Ascencio-Ibanez, Jose Trinidad, Sozzani, Rosangela, Lee, Tae-Jin et al.</a> Global analysis of Arabidopsis gene expression uncovers a complex array of changes impacting pathogen response and cell cycle during geminivirus infection.	PLANT PHYSIOLOGY	<a href="#">AT1G01010</a> ; <a href="#">AT1G01030</a> ; <a href="#">AT1G01040</a> ; <a href="#">AT1G01060</a> ; <a href="#">AT1G01080</a> ; <a href="#">AT1G01090</a> ; <a href="#">AT1G01120</a> ; <a href="#">AT1G01140</a> ; <a href="#">AT1G01190</a> ; <a href="#">AT1G01290</a> ; <a href="#">AT1G01300</a> ; <a href="#">AT1G01320</a> ; <a href="#">AT1G01340</a> ; <a href="#">AT1G01350</a> ; <a href="#">AT1G01430</a> ; <a href="#">AT1G01470</a> ; <a href="#">AT1G01550</a> ; <a href="#">AT1G01560</a> ; <a href="#">AT1G01620</a> ; <a href="#">AT1G01725</a> ; ...more	2008
<a href="#">Mahé, Laetitia, Combes, Marie-Christine, Lashermes, Philippe et al.</a> Comparison between a coffee single copy chromosomal region and Arabidopsis duplicated counterparts evidenced high level synteny between the coffee genome and the ancestral Arabidopsis genome.	PLANT MOLECULAR BIOLOGY	<a href="#">AT1G01110</a> ; <a href="#">AT1G01140</a> ; <a href="#">AT1G03800</a> ; <a href="#">AT1G04080</a> ; <a href="#">AT1G04150</a> ; <a href="#">AT1G04160</a> ; <a href="#">AT1G04190</a> ; <a href="#">AT1G04210</a> ; <a href="#">AT1G04220</a> ; <a href="#">AT1G04440</a> ; <a href="#">AT1G05460</a> ; <a href="#">AT1G08840</a> ; <a href="#">AT1G16800</a> ; <a href="#">AT1G19440</a> ; <a href="#">AT1G22610</a> ; <a href="#">AT1G25450</a> ; <a href="#">AT1G27770</a> ; <a href="#">AT1G30270</a> ; <a href="#">AT1G34320</a> ; <a href="#">AT1G51570</a> ; ...more	2007
<a href="#">Schmidt, Ulrike G., Endler, Anne, Schelbert, Silvia et al.</a> Novel Tonoplast Transporters Identified using a Proteomic Approach with Vacuoles Isolated from Cauliflower Buds.	PLANT PHYSIOLOGY	<a href="#">AT1G01790</a> ; <a href="#">AT1G04630</a> ; <a href="#">AT1G04750</a> ; <a href="#">AT1G06470</a> ; <a href="#">AT1G08480</a> ; <a href="#">AT1G09330</a> ; <a href="#">AT1G10950</a> ; <a href="#">AT1G16390</a> ; <a href="#">AT1G16780</a> ; <a href="#">AT1G17840</a> ; <a href="#">AT1G19910</a> ; <a href="#">AT1G26310</a> ; <a href="#">AT1G27770</a> ; <a href="#">AT1G29310</a> ; <a href="#">AT1G32210</a> ; <a href="#">AT1G32400</a> ; <a href="#">AT1G34610</a> ; <a href="#">AT1G42960</a> ; <a href="#">AT1G53210</a> ; <a href="#">AT1G53840</a> ; ...more	2007

# Functions of Arabidopsis orthologs

*Plant Physiology*<sup>®</sup>

Issues Advance Articles More Content ▼ Submit ▼ Purchase About ▼

Plant Physiology

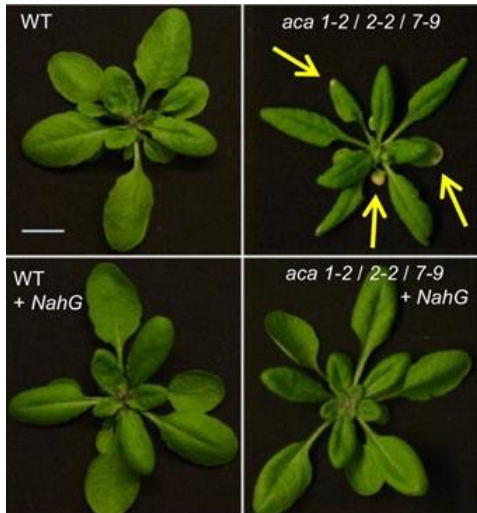


Volume 185, Issue 4

JOURNAL ARTICLE

## Arabidopsis $\text{Ca}^{2+}$ -ATPases 1, 2, and 7 in the endoplasmic reticulum contribute to growth and pollen fitness <sup>FREE</sup>

Maryam Rahmati Ishka ✉, Elizabeth Brown, Alexa Rosenberg, Shawn Romanowsky, James A Davis, Won-Gyu Choi, Jeffrey F Harper ✉ [Author Notes](#)

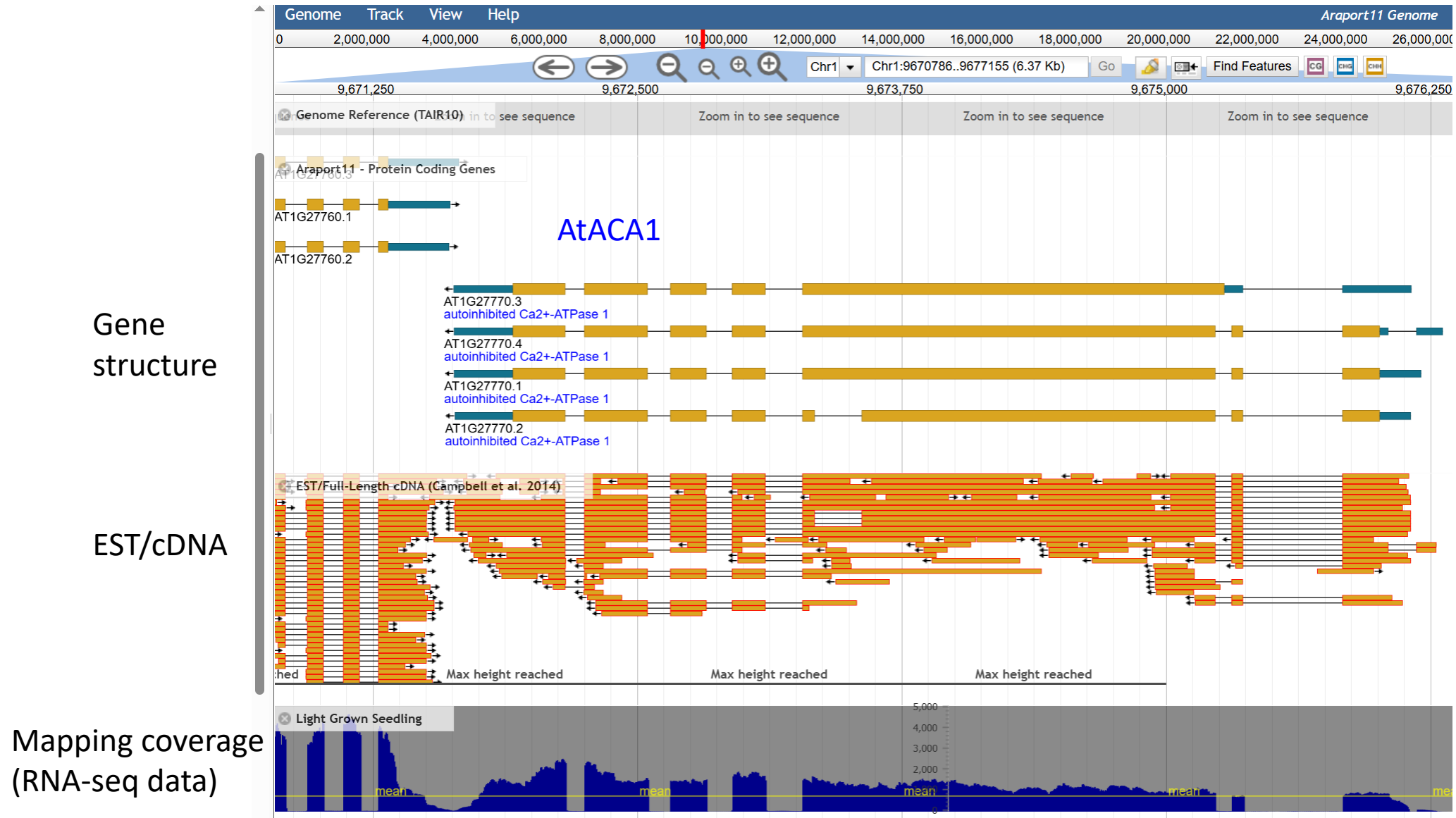


SA-dependent rosette size reductions and leaf lesions

### Abstract

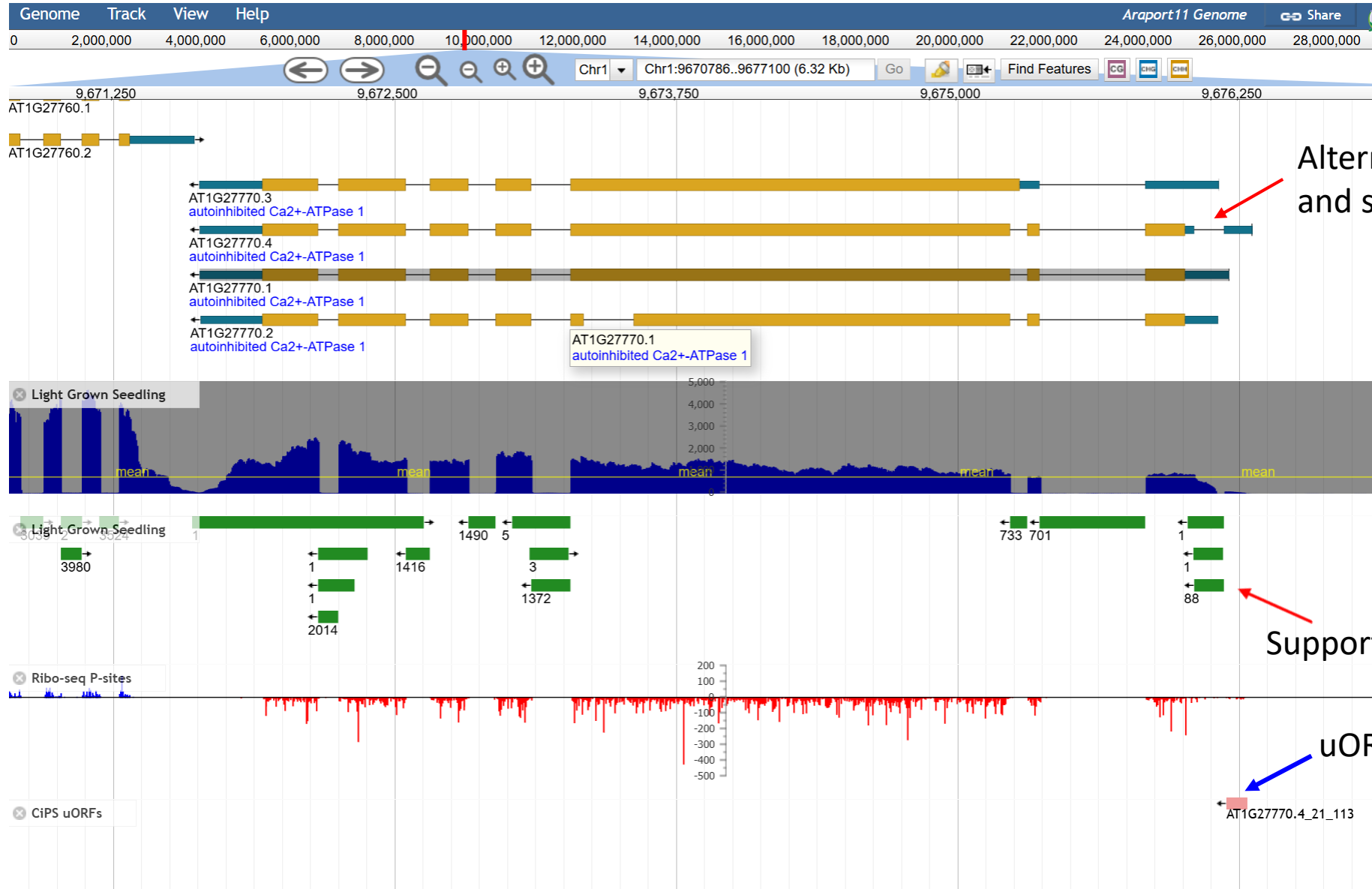
Generating cellular  $\text{Ca}^{2+}$  signals requires coordinated transport activities from both  $\text{Ca}^{2+}$  influx and efflux pathways. In Arabidopsis (*Arabidopsis thaliana*), multiple efflux pathways exist, some of which involve  $\text{Ca}^{2+}$ -pumps belonging to the Autoinhibited  $\text{Ca}^{2+}$ -ATPase (ACA) family. Here, we show that ACA1, 2, and 7 localize to the endoplasmic reticulum (ER) and are important for plant growth and pollen fertility. While phenotypes for plants harboring single-gene knockouts (KOs) were weak or undetected, a triple KO of *aca1/2/7* displayed a 2.6-fold decrease in pollen transmission efficiency, whereas inheritance through female gametes was normal. The triple KO also resulted in smaller rosettes showing a high frequency of lesions. Both vegetative and reproductive phenotypes were rescued by transgenes encoding either ACA1, 2, or 7, suggesting that all three isoforms are biochemically redundant. Lesions were suppressed by expression of a transgene encoding NahG, an enzyme that degrades salicylic acid (SA). Triple KO mutants showed elevated mRNA expression for two SA-inducible marker genes, *Pathogenesis-related1* (PR1) and PR2. The *aca1/2/7* lesion phenotype was similar but less severe than SA-dependent lesions associated with a double KO of vacuolar pumps *aca4* and *11*. Imaging of  $\text{Ca}^{2+}$  dynamics triggered by blue light or the pathogen elicitor flg22 revealed that *aca1/2/7* mutants display  $\text{Ca}^{2+}$  transients with increased magnitudes and durations. Together, these results indicate that ER-localized ACAs play important roles in regulating  $\text{Ca}^{2+}$  signals, and that the loss of these pumps results in male fertility and vegetative growth deficiencies.

# Gene structure and alternative splicing





# Alternative splicing and uORFs



## Alternative TSS and splice junction

Splice  
junction  
(RNA-seq)

## Ribo-seq P site

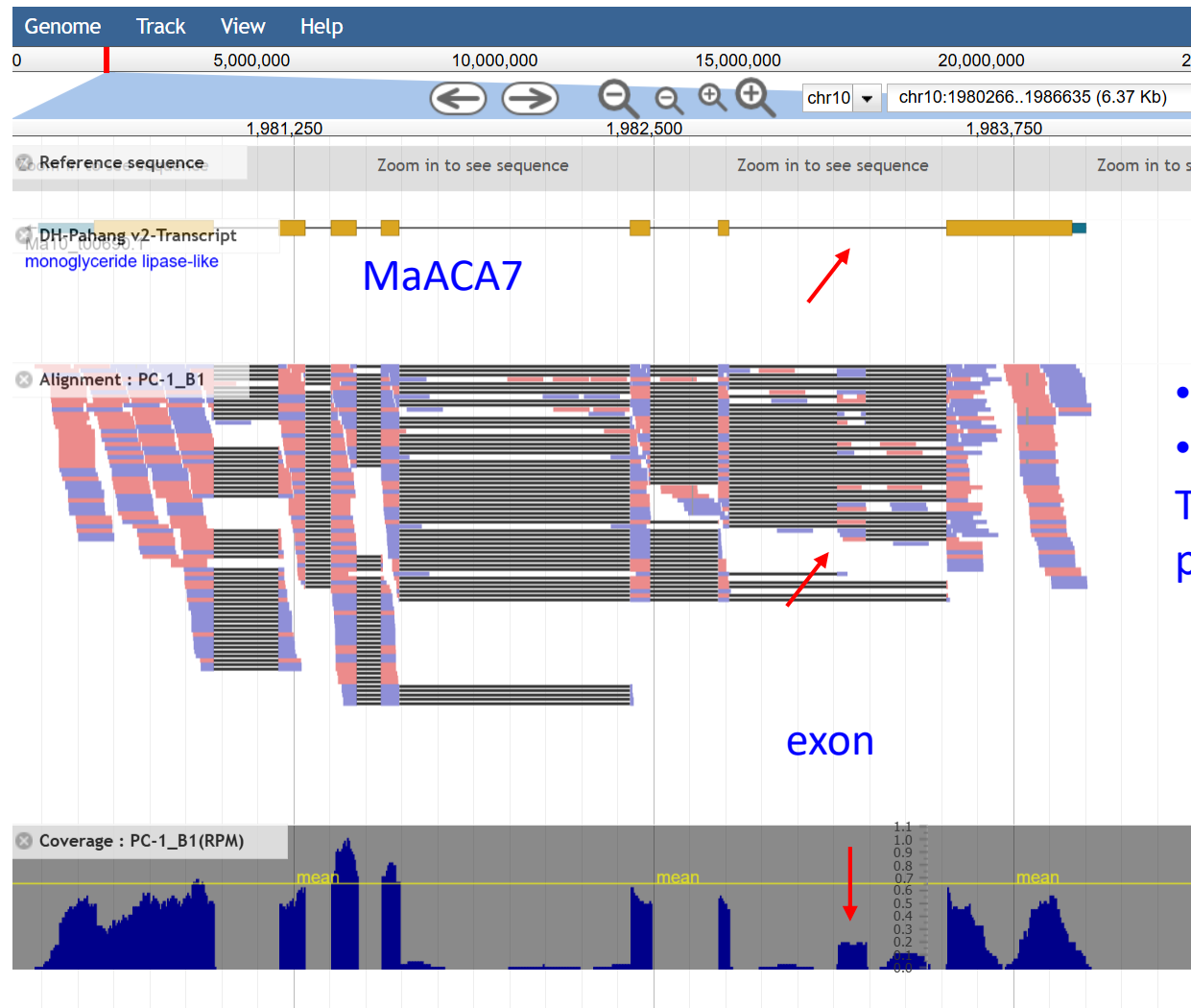
## Support model 4

uORF

# In-house Jbrowse of banana: gene model

Alignment  
(RNA-seq data)

Mapping coverage  
(RNA-seq data)



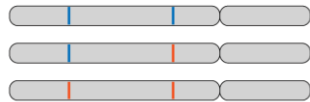
- Alternative splicing
  - AAA genome
- Three copies may not produce identical transcripts



# In-house Jbrowse of banana: sequence polymorphism

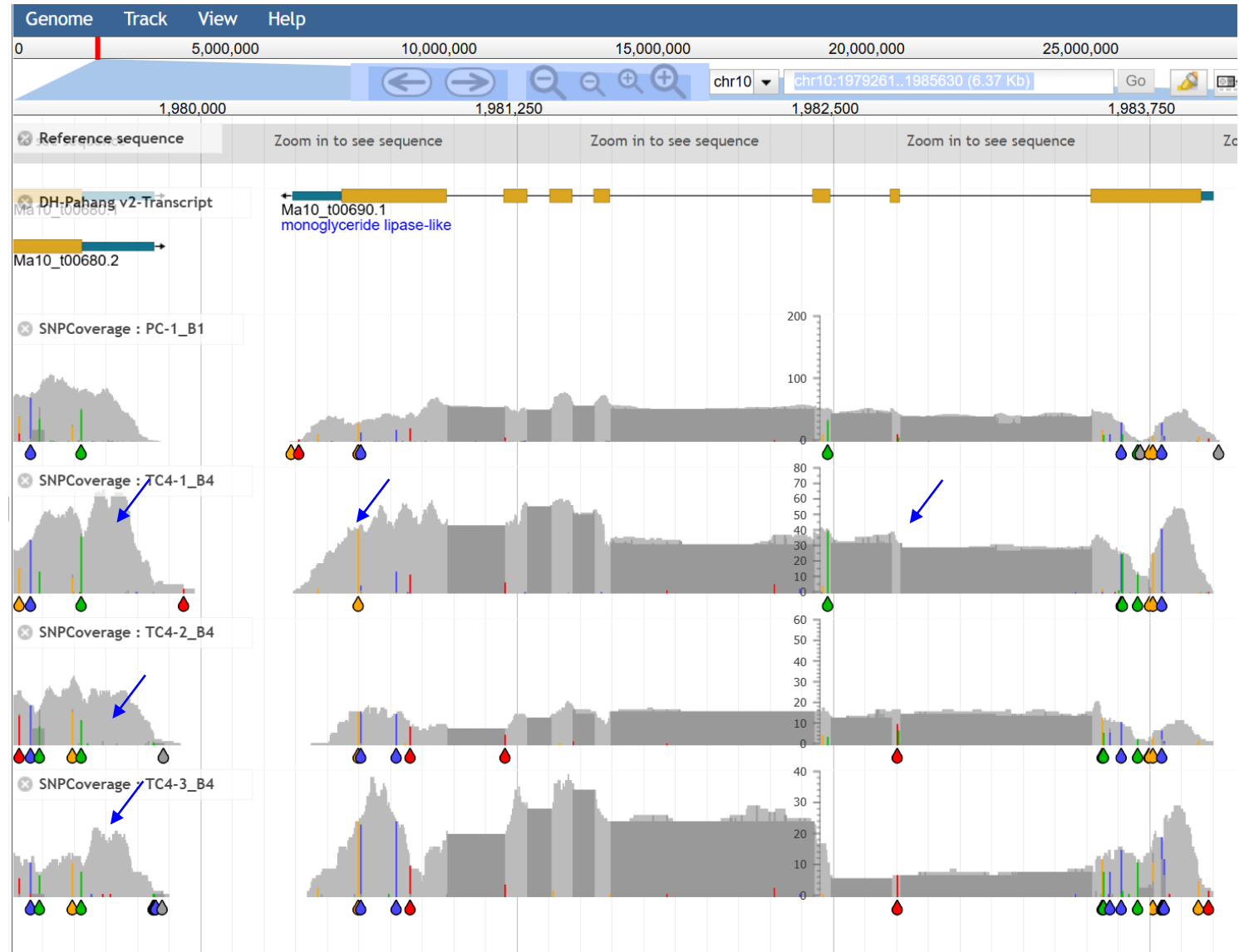
● Reference

● Alternative



Allele depth

10,5 5,10

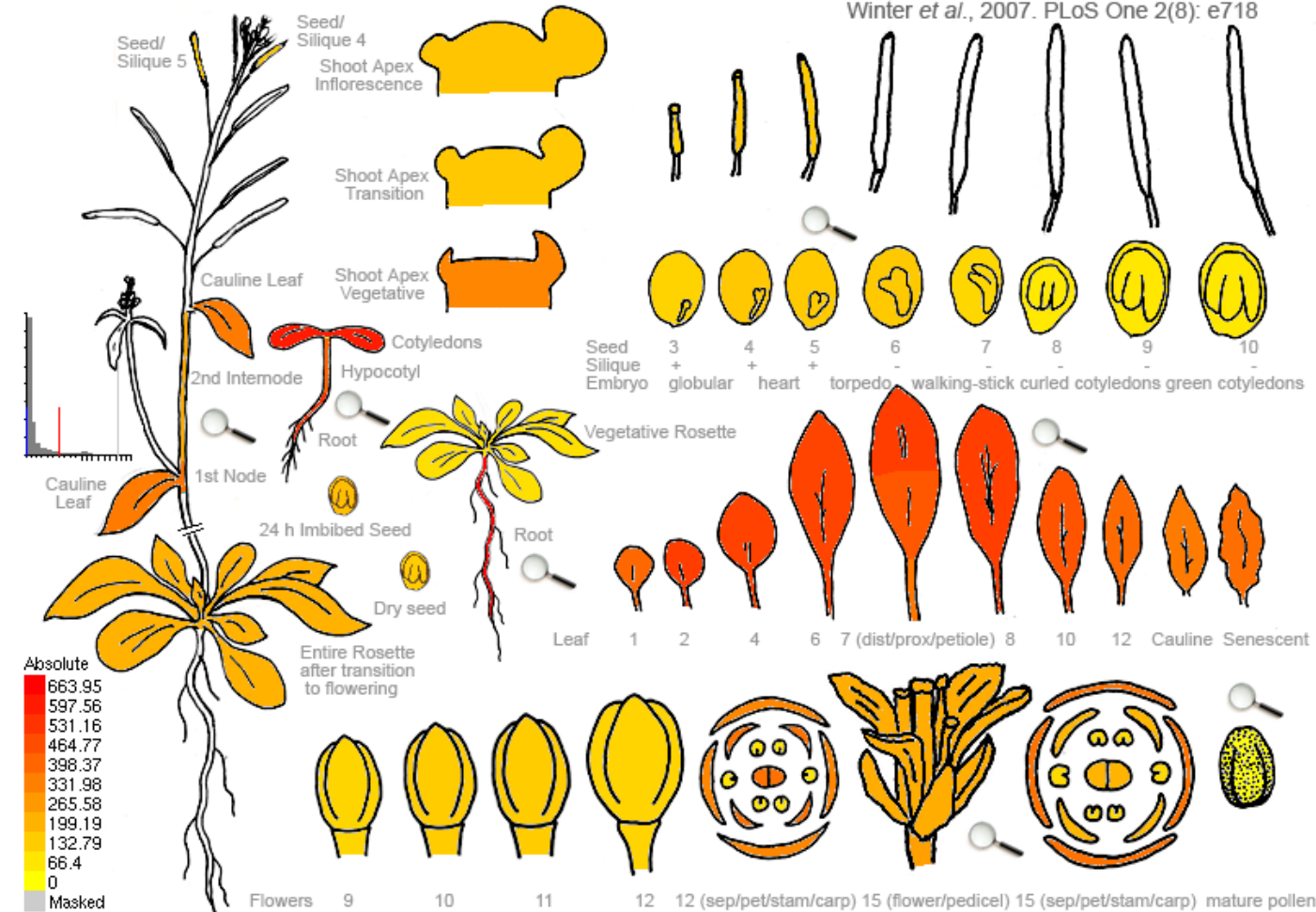


# Locus page: Development map expression

At1g27770 261650\_at

Arabidopsis eFP Browser at bar.utoronto.ca

Winter et al., 2007. PLoS One 2(8): e718



eFP Browser by B. Vinegar, drawn by J. Alls and N. Provart. Data from Gene Expression Map of Arabidopsis Development: Schmid et al., 2005, Nat. Gen. 37:501, and the Nambara lab for the imbibed and dry seed stages. Data are normalized by the GCOS method, TGT value of 100. Most tissues were sampled in triplicate.

# Abiotic and biotic stresses

## Biotic Stress

### Abiotic Stress II

### Abiotic Stress

### Biotic Stress II

## Biotic Stress

### Chemical

### Developmental\_Map

### Developmental\_Mutants

### Development\_RMA

### Germination

### Guard\_Cell

### Hormone

### Klepikova\_Atlas

### Lateral\_Root\_Initiation

### Light\_Series

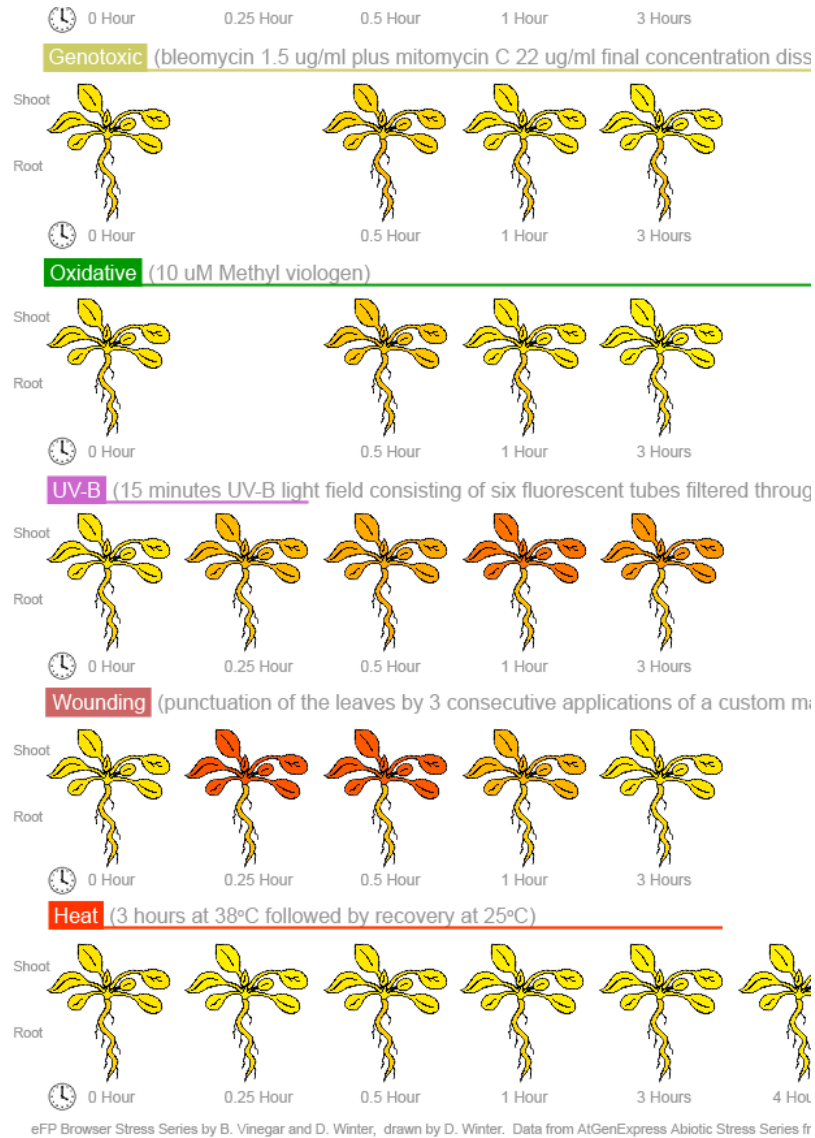
### Natural\_Variation

### Regeneration

### Root\_II

### Root

### Seed



At1g27770 261650\_at

*Botrytis cinerea*



Conidiospores (Diluted to 5X10<sup>5</sup> spores/ml)

Mock Treatment (Potato Dextrose Broth)

Control

18 Hours

48 Hours

Half Leaf *Pseudomonas syringae*

Mock Treatment (10mM MgCl<sub>2</sub> solution)

Avirulent pathogen (ES4326 avrRpt2)

Virulent pathogen (ES4326)

ALL SAMPLES 24 & 48 Hour Injection

4 Hour Injection

8 Hour Injection

16 Hour Injection

4 Hours

8 Hours

16 Hours

24 Hours

48 Hours

Infiltrating *Pseudomonas syringae*

Mock Treatment (10 mM MgCl<sub>2</sub>)

Virulent (10<sup>8</sup> cfu/ml pv. tomato DC3000)

Avirulent (10<sup>8</sup> cfu/ml pv. tomato avrRpm1)

INJECTION 24 Hour Sample

2 Hour Sample

6 Hour Sample

2 Hours

6 Hours

24 Hours

2 Hours

6 Hours

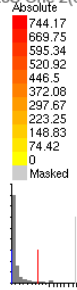
24 Hours

Arabidopsis eFP Browser at bar.utoronto.ca

Winter et al., 2007. PLoS One 2(8): e718

- Plant material from the leaves of 4 week old wild-type *Arabidopsis thaliana* plants of Columbia-0 ecotype was analyzed
- Leaves were inoculated by placing 4 5- $\mu$ l drops of the solution on each leaf
- Plants grown under 12/12 hour light/dark conditions
- All measurements were taken in triplicates - the average of which is shown
- RNA was isolated and hybridized to the ATH1 GeneChip
- The data were normalized by GCOS normalization, TGT 100
- This study is part of the AtGenExpress project, funded by the NSF

Results provided by the Ausubel Lab



- Plant material from the leaves of 4 week old wild-type *Arabidopsis thaliana* plants of Columbia-0 ecotype was analyzed
- Half of a plant leaf was injected while the other half was collected on a time course for analysis
- Plants grown under 16/8 hour light/dark conditions
- All measurements were taken in triplicates - the average of which is shown
- RNA was isolated and hybridized to the ATH1 GeneChip
- The data were normalized by GCOS normalization, TGT 100
- This study is part of the AtGenExpress project, funded by the NSF

Results provided by the Dong Lab

- Plant material from the leaves of 5 week old wild-type *Arabidopsis thaliana* plants of Columbia-0 ecotype was analyzed
- Plants grown under 8/16 hour light/dark conditions but transferred to 16/8 hour light/dark conditions for the experiment
- All measurements were taken from infiltrated leaves in triplicates - the average of which is shown
- RNA was isolated and hybridized to the ATH1 GeneChip
- The data were normalized by GCOS normalization, TGT 100
- This study is part of the AtGenExpress project, funded by the DFG

Results provided by the Nürnberger Lab

Typell-Secretion System Deficient (10<sup>8</sup> cfu/ml pv. tomato DC3000 hrcC-)

Nonhost Bacteria (10<sup>8</sup> cfu/ml pv. phaseolicola)

# Hormone response


Locus: AT1G27770 (ACA1)  Premium Page

[system](#) [stamen](#) [stem](#) [vascular leaf](#)

## BAR eFP Browser

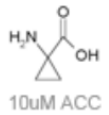
Data Source Hormone

At1g27770 261650\_at

 = Control

ACC

Mock Treatment



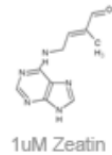
30 Minutes

1 Hour

3 Hours

Zeatin

Mock Treatment



30 Minutes

1 Hour

3 Hours

IAA

Mock Treatment



ABA

Mock Treatment



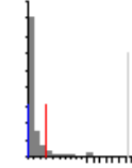
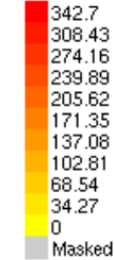
Methyl Jasmonate

Mock Treatment



Arabidopsis eFP Browser at bar.utoronto.ca  
Winter et al., 2007. PLoS One 2(8): e718

Absolute



### 3 suggestions for next-generation researchers

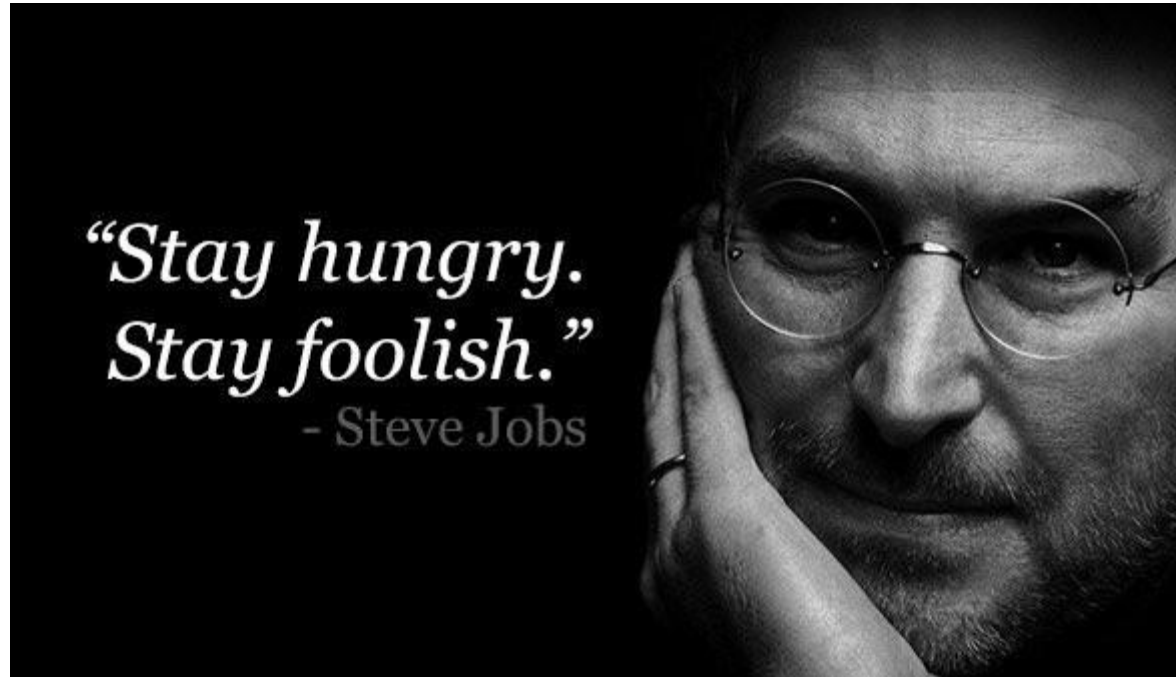
Play like a kindergarten child (no need to read the whole manual)

**Warning:** For molecular biology experiments, DO read the whole protocol carefully



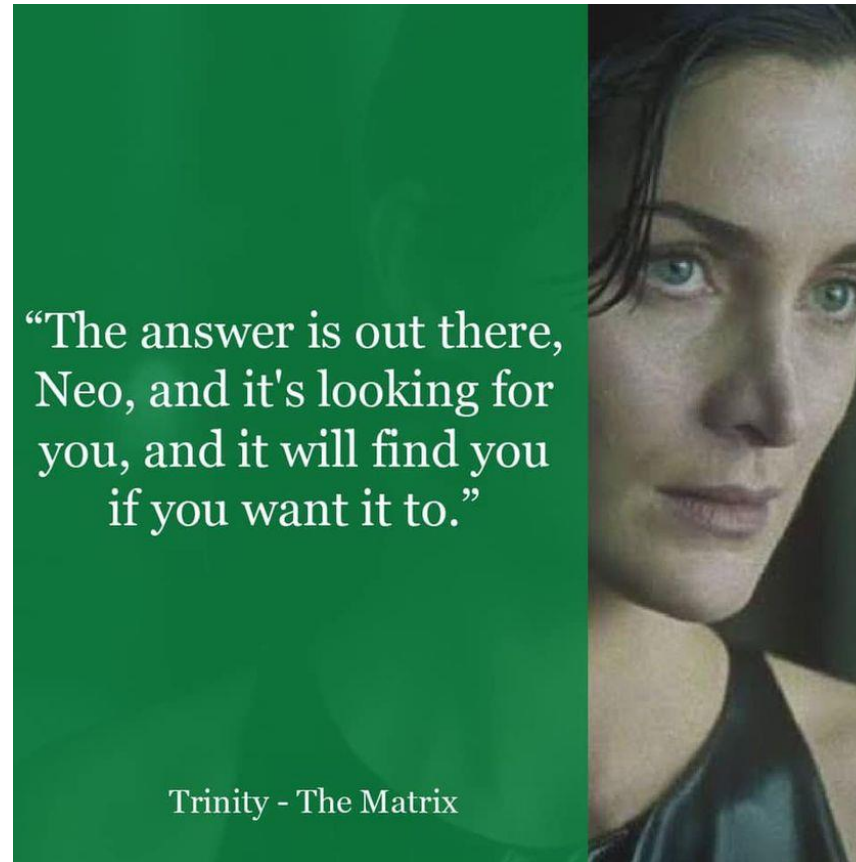
<https://tw.123rf.com/>

## Suggestions for next-generation researchers



(ask as many questions as possible; it is free)

## Suggestions for next-generation researchers

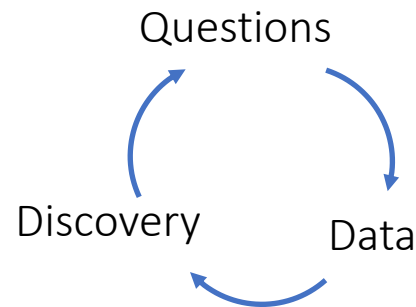


<https://www.facebook.com/thematrixquotes/>



# Questions for TAIR

- **To what extent is known for the gene of your interest?**
  - DNA, RNA, protein sequences, isoforms
  - Functions and cellular localization (predicted, supported by experimental evidence)
  - Gene expression (spatial, temporal, response to stress, hormone ...)
  - Others: mutants, small RNAs, RNA degradation, ribosome footprints and DNA methylation
- **Are there other genes having similar features as the gene of your interest?**
  - Similar DNA, RNA, protein sequences
  - Similar functions
  - Similar expression pattern
  - ....



# Exercise II

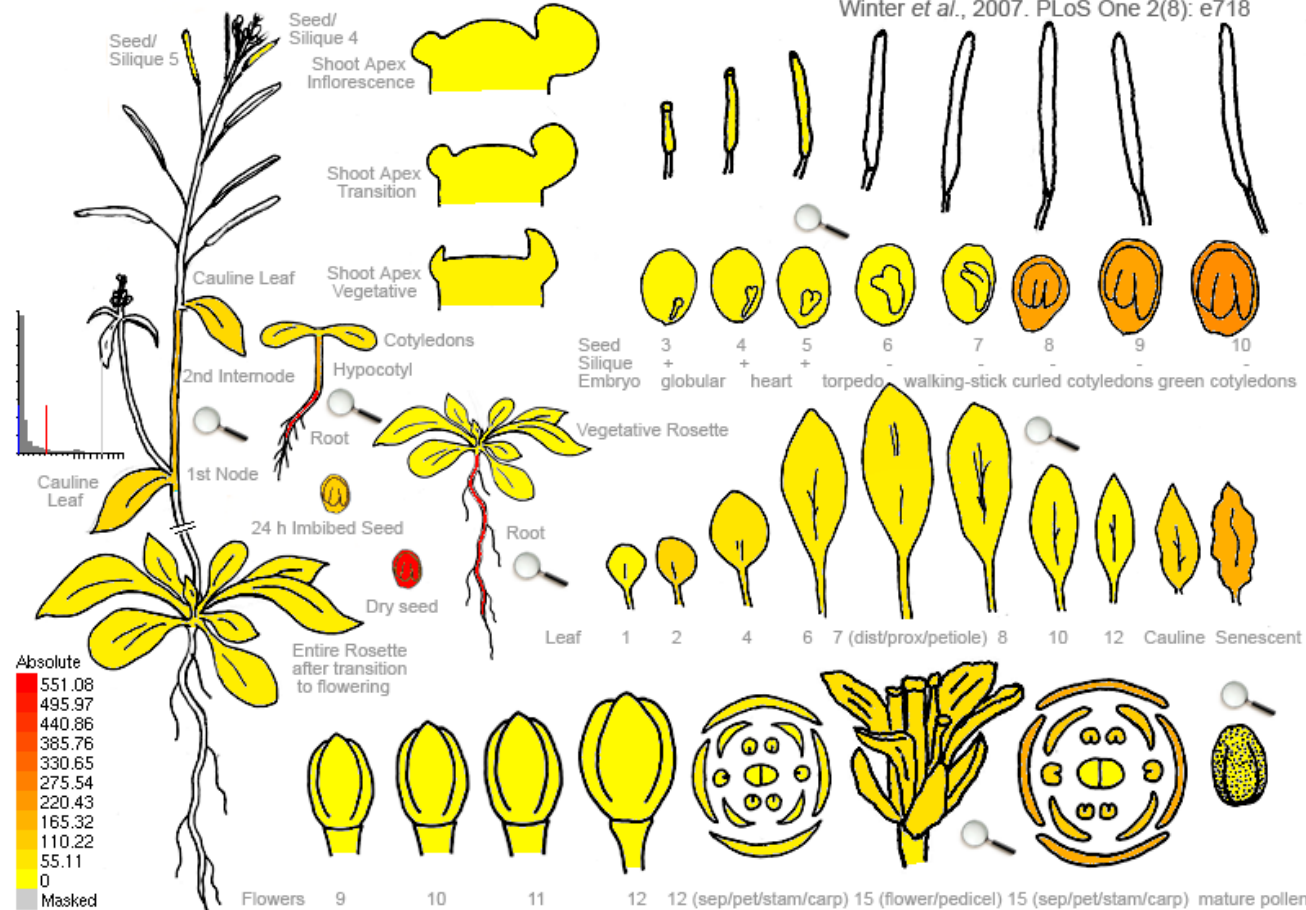
## **TGA1 (AT5G65210)**

1. GO biological process: number of keywords?; number of loci in each keyword?
2. In annotation, what functions are supported by experimental results?
3. RNA expression: highest in which tissue, at what stage, in which ecotype?  
diurnal gene? response to any stress or hormone?

At5g65210 247199\_at

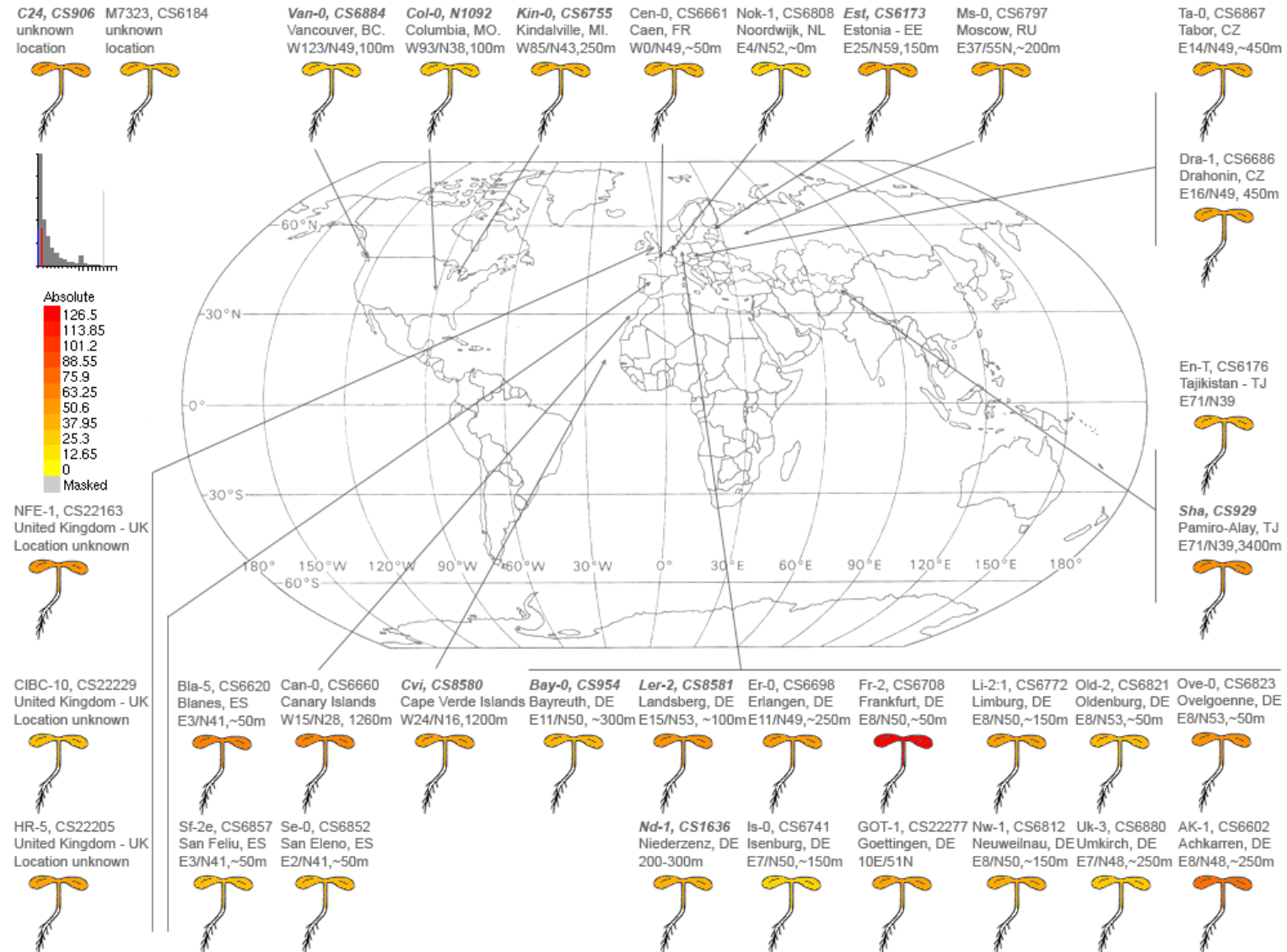
Arabidopsis eFP Browser at bar.utoronto.ca

Winter et al., 2007. PLoS One 2(8): e718



eFP Browser by B. Vinegar, drawn by J. Alls and N. Provart. Data from Gene Expression Map of Arabidopsis Development: Schmid et al., 2005, Nat. Gen. 37:501, and the Nambara lab for the imbibed and dry seed stages. Data are normalized by the GCOS method, TGT value of 100. Most tissues were sampled in triplicate.

Natural Variation eFP Browser. Data from the Weigel Lab (Lempe *et al.*, 2005, PLoS Genetics 1:e6). Aerial parts of 4 day old seedlings greenhouse-grown in soil at 23C under continuous light were sampled. Data normalized by the GCOS method, TGT value of 100. Plant material sampled in triplicate where *indicated by italics*, otherwise once.





Thank you !

For questions, you can contact

Ho-Ming Chen 陳荷明

Office: Agricultural Technology Building A638

Email: [homing@as.edu.tw](mailto:homing@as.edu.tw)

Phone: 2787-2073